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Minimum DB seq length: 0
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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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1: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
2: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
3: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1982.DAT:*
3: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1983.DAT:*
5: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1984.DAT:*
6: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1985.DAT:*
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7 188.488 Million cell updates/sec
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                                                                                                                                  /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1989.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

9	8	7	6	υī	4	w	2	1	Result
291	291	291	291	291	298	298	298	298	Score
95.7	95.7	95.7	95.7	95.7	98.0	98.0	98.0	98.0	% Query Match
57	57	57	57	57	57	57	57	57	Query Match Length DB
20	14	14	14	13	20	20	17	11	B
AAY06670	AAR39312	AAR33850	AAR41280	AAR28298	AAY03208	AAY06665	AAR95267	AAR05238	ID
Nisin Z of Lactoba	. Lactococcal bacter	Bacteriocin LL-2 p	Bacteriocin. Lact	Sequence encoded b	Amino acid sequenc	. Nisin A of Lactoba	Pre-nisin A. Lact	Nisin precursor pr	Description

PXR

05-JUL-1988; 88US-0214959. (UYMA-) UNIV OF MARYLAND.

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	<u>1</u>	17	16	15	14	13	12	11	10
81.5		82				4.	٠	٠.	4.	94.5	96	96	97	97	97	97	104	104	104	104	105	128	157	157	157	157	157	176	178	181	185	185	185	185	185
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35	47	34	34	34	34	52	52	52	52	51	34	34	34	34	34	34	34	34	34	34	34	39	56	56	56	56	56	34	34	41	34	34	34	34	34
18	16	14	14	14	21	20	20	14	5	24	23	14	23	23	17	13	17	15	14	14	14	18	24	21	20	19	11	20	14	18	24	23	21	19	15
AAY31660	AAR85080	AAR30171	AAR41281	$\mathbf{r}$	AAB11032	AAY03210	ŭ	731	349	N	77	AAR50954	77	AAU75775	AAR95245	AAR28299	26	AAR56162	AAR43272	AAR37314	AAR50953	AAY31658	ABU59621	AAY91744	20	AAW66445	23	AAW84352	AAR43070	AAY31659	ABU59619	9097	174	AAW66443	AAR62635
lantibioti	Hyicin M51 (lanthi	iocin	n (Gene	bacte	Lactococcus lactis	Amino acid sequenc	S. epidermis readi	3S	re-e	Streptococcus muta	occus lac	0	occus lacti	Lactococcus lactis	Nisin 2. Lactococ	o	5	Sequence of the ba	$\sim$	Epidermin. Staphy			Cationic cancer -t	Cationic peptide S	Amino acid sequenc	Cationic peptide s	'n		Lactococcus lactis	Subtilin-nisin chi	ic cancer	an	c peptide	G	Ф ш.

## ALIGNMENTS

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	30-JUN-1989;		25-JAN-1990.		WO9000558-A.			Protein			Peptide	Key		Streptococcus 1		post-translation	Nisin precurson	,	Streptococcus 1	Nisin precurson		04-AUG-1990 (f		AAR05238;		AAR05238 standa	RESULT 1 AAR05238
	89WO-US02820.						/note="nisin precursor peptide"	2457	translational modification"	/note="leader fragment responsible for inducing post-	123	Location/Qualifiers		Streptococcus lactis ATCC 11454.		post-translational modification; Streptococcus lactis ATCC 11454;	Nisin precursor peptide; nisin leader peptide;		Streptococcus lactis ATCC 11454.	Nisin precursor protein and leader peptide encoded by DNA derived from		(first entry)				AAR05238 standard; protein; 57 AA.	

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Best Local S
Matches 56
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The gene cluster nisABTCIPRK (see AAT29660 and AAT29661) of Lactococcus lactis includes the nisA gene coding for pre-nisin A (AAR95267, see also AAR95263) and the genes for nisin modification, secretion and immunity. nisB (AAR95268) and nisC (AAR95270) are believed to be involved in reactions that modify pre-nisin; nisT (AAR95269) is
                                                                                            Making cell which expresses nisin but does gene - by providing cell with variant nish modification, secretion and immunity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The leader peptide assists in inducing post-translational modification a protein precursor when attached to the precursor as a leader. The precursor polypeptide contains Ser, Thr and Cys which undergo modification after translation to arrive at the the mature protein , having unusual amino acids. Tag a is claimed in the patent.
                                                                    Disclosure; Fig 7; 69pp; English.
                                                                                                                                                N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-AUG-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR95267;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR95267 standard;
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N-PSDB; AAQ93354.
                                                                                                                                                                                   Dodd HM,
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                                                                                                                                                                                                                                                                                                                                          Peptide
                                                                                                                                                                                                                                                                                                                                                       Key
                                                                                                                                                                                                                                                                                                                                                                            Lactococcus lactis strain NIZO R5.
                                                                                                                                                                                                                                                                                                                                                                                                               Nisin A; nisA gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Leader peptide sequence - including post-translational modification
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                                                                                                                                                                                                         (BIOT-) BIOTECHNOLOGY & BIOLOGICAL SCI RES COUNC
                                                                                                                                                                                                                                                                                                                                                                                                    lantibiotic;
                                                                                                                                              1996-268616/27.
DB; AAT29660.
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ilarity 98.2%;
Conservative
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/label= Sig_peptide
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                                                                                                                                                                                                                                                                                                                                                                                                    antimicrobial; preservative; antibiotic;
n engineering.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               entry)
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.9e-29;
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                                                                                                         gene,
                                                                                                          contain natural nisA
e, and genes for nisin
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                                                                                                         genes
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Best Local S
Matches 56
                                                                                                                                                                 nis A gene (see AAX87792). Nisin A is lanthionine-containing bacteriocin. The invention relates to methods of enhancing performance in an animal by administering a bacterium capable of expressing a performance enhancing polypeptide such as misin A or nisin Z. The enhanced performance results in improved growth rates and feed conversion efficiencies. The bacterium, which may be genetically modified to express the performance enhancing polypeptide, is administered to the gastrointestinal tract, especially to an embryo or meonatal animal. If the polypeptide is nisin, it may also inhibit ruminal methane, decrease acetate to propionate ratios and prevent amino acid deamination.

Administration of an appropriate bacterium which may act as a manimal methane.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel performance enhancing method resulting in improved rates and feed conversion efficiencies in animals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nisin A; nis A; lantibiotic; feed conversion; probiotic;
                                                                                   probiotic may also help control enteric pathogens in poultry, polypeptide is produced continuously in the gut, maintaining constant level. The protein is eventually degraded, leaving
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 61; 79pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence represents the nisin A precursor peptide Lactobacillus lactis NIZO R5. The sequence is deduced from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-FEB-1998;
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                                                              residues
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DB; AAX87792.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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Pred. No. 9.9e-29;
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Sequence

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AAXO3208
ID AAYO
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XX AAYO
DT O3-A
XX AMIN
XX Subl
KW Gram
XX Subl
KW Gram
XX WO99
XX UNKN
XX UN
RESULT 5
AAR28298
ID AAR2
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AC AAR2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This is the amino acid sequence of nicin A used in the method of the invention involving the use of prosublancin 168. The peptide designated sublancin 168, is an antimicrobial useful for treating infections and preserving food against spoilage bacteria, particularly Gram-positive bacteria. Pro-sublancin 168 and pre-sublancin 168, are the precursors of sublancin 168. Sublancin 168 is very stable at low pH and can be autoclaved without damage. It does not decompose after 2 years in aqueous solution of about
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New antimicrobial peptide, sublancin 168, from Bacillus subtilis used for, e.g. treatment of infections caused by Gram negative bacteria and as food preservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hansen JN;
  25-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1999-131752/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sublancin 168; antimicrobial; food preservative; Gram-positive bacteria; pre-sublancin 168; nicin
                                                     AAR28298;
                                                                                                         AAR28298 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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                                                                                                                                                                                                                                                                        MSTKDFNLDLVSVSKKDSGASPRITSTSLCTPGCKTGALMGCNMKTATCHCSIHVSK 57
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                                                                                                                                                                                                                                           MSTKDFNLDLVSVSKKDSGASPRITSISLCTPGCKTGALMGCNMKTATCHCSIHVSK 57
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nilarity 98.2%;
Conservative
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(updated)
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                                                                                                                                                                                                                                                                                                                                                    Score 298; DB 20;
Pred. No. 9.9e-29;
0; Mismatches 1
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Pred. No. 9.9e-29;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                          Length 57;
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                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                             Total DNA was isolated from the L. lactis strains NIZO 22186 and NIZO R5. With the aid of the nisA gene of strain NIZO R5 as a probe, a 4.5 kb HindIII fragment was identified in the total DNA strain NIZO 22186, which was then cloned in M13 mpl8. The DNA sequence of the gene for nisin Z production (nisZ) was determined by making use of oligos complementary to the 5' and 3' flanking sequences of the nisA gene. The nucleotide sequence the nisA gene is found to be identical to that of the nisA gene with the exception of a C to A transversion in posn. 148 which results in the replacement of AA this27 by Asn27. The above indicate that the structure of nisin Z is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New lantiobiotic cpds. related to nisin A - and Lactococcus strains which produce them, useful as preservatives for foods and animal feeds
           Lactococcus lactis
                                                                     Bacteriocin
                                                                                             25-MAR-2003
10-MAR-1994
                                                                                                                                AAR41280;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Key
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                                 Bacteriocin;
inhibit.
                                                                                                                                                        AAR41280 standard; Protein;
                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example; Fig 3; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1992-382116/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            De Vos WM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-APR-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09-APR-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29-OCT-1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lactococcus lactis
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on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kuipers OP,
                                                                                                                                                                                                                                                                                                                 57 AA;
                                                                                                                                                                                                                                                                  Conservative
                                             LL-2; gram
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nisin Z;
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                                                                                           (updated)
(first entry)
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                                                                                                                                                                                                                                                                            95.7%;
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                                             positive
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                                                                                                                                                                                                                                                                           Score 291; DB 1:
Pred. No. 7e-28;
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                                                                                                                                                                                                                                                                 Mismatches
                                              bacteria; antimicrobial;
                                                                                                                                                                                                                                                                                         DB 13;
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Best Local S
Matches 55
                                                                                                                         encoded protein inhibits selected gram positive bacteria and this property is enhanced if further purified by HPLC. The materials being treated to provide inhibition are preferably foods, although other materials may be treated.
                                                                                                                                              The sequence (AAQ49150) was amplified using primers (AAQ49151-52). encoded protein inhibits selected gram positive bacteria and this property is enhanced if further purified by HPLC. The materials
                                                                                                                                                                                                                                                                                                                                                                                               US5232849-A.
                                                                                   Sequence
                                                                                                                                                                                        Disclosure; Page 13-14 (col 15,16,17,18); 14pp; English
                                                                                                                                                                                                            Bacteriocin from Lactococcus lactis subspecies lactis - inhibitory against Gram-positive bacteria
                                                                                                                                                                                                                                              WPI; 1993-287077/36.
N-PSDB; AAQ49150.
                                                                                                                                                                                                                                                                            Henderson JT,
                                                                                                                                                                                                                                                                                                                      01-JUL-1991;
14-MAY-1992;
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                                                    Similarity
           MSTKDFNLDLVSVSKKDSGASPRITSTSLCTPGCKTGALMGCNMKTATCHCSIHVSK 57
                                                                                                     on 25-MAR-2003
on 25-MAR-2003
MSTKDFNLDLVSVSKKDSGASPRITSISLCTPGCKTGALMGCNMKTATCNCSIHVSK 57
                                                                                 57 AA;
                                          Conservative
                                                                                                                                                                                                                                                                                                 INT FLAVORS & FOOD INGREDIENTS CO.
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92US-0882079.
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/note=
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/note=
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24..57
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/note= "Claim 3"
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                                                  95.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "The CH2 in the side chain joins the S in residue 30"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "The CH2 in the side chain joins the S in residue 51"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "The CH2 in the side chain joins the S in residue 34"
                                                                                                                                                                                                                                                                                                                                                                                                                    "The S joins the side chain of residue
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "The S joins the side chain of residue
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                                                                                                       correct PF field.)
                                                                                                                                                                                                                                                                             Van WASSENAAR PD,
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                                       Score 291; DB 14;
Pred. No. 7e-28;
1; Mismatches 1;
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RESULT 7

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RESULT 8
AAR39312
ID AAR3
XX
AC AAR3
XY
DT 25-M
DT 21-J
XX
XX
XX
DE Lact
XX
XX
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XX
XX
XX
XX
XX
OS Lact
XX
OS Lact
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                                                                                                                                                                                                                              Query Match
Best Local S
Matches 55
                                                                                                                                                                                                                                                                                           The sequence is that of bacteriocin LL-2 precursor which can be used in a method for the inhibition of Gram-positive bacteria. LL-2 is especially useful for treatment of food, although other non-food materials may also be treated. (Updated on 25-MAR-2003 to correct PA field.)
         Lactococcus lactis (subspecies lactis)
                                Bacteriocin;
                                                                         25-MAR-2003
21-JAN-1994
                                                                                                           AAR39312;
                                                                                                                               AAR39312 standard;
                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 13; 14pp; English
                                                                                                                                                                                                                                                                                                                                                                                           Inhibition of Gram-positive bacteria - using bacteriocin derived from Lactococcus lactis sub-species lactis NRRL B-18809
                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1993-017533/02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Vedamuthu ER,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUL-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUL-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22-DEC-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lactococcus lactis sub-species lactis NRRL B-18809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Food treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteriocin LL-2 precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-MAR-2003
12-MAY-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR33850;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR33850 standard; Protein; 57
                                                     Lactococcal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US5173297-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (UNIL ) QUEST
                                                                                                                                                                                                                               55
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                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                              AAQ34782.
                                                                                                                                                                                                 MSTKDFNLDLVSVSKKDSGASPRITSTSLCTPGCKTGALMGCNMKTATCHCSIHVSK 57
                                                                                                                                                                                     MSTKDFNLDLVSVSKKDSGASPRITSISLCTPGCKTGALMGCNMKTATCNCSIHVSK
                                                                                                                                                                                                                                                                        57 AA;
                                                                                                                                                                                                                             95.7%;
ilarity 96.5%;
Conservative
                                                   bacteriocin polypeptide precursor.
                             inhibition; polypeptide; Lactococcus lactis.
                                                                         (updated)
(first en
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (updated)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INT FLAVORS & FOOD INGREDIENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Henderson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    91US-0721774.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            91US-0721774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /*note= "signal peptide"
24..57
/*note= "mature peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                Protein;
                                                                          entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ŢŢ,
                                                                                                                                57
                                                                                                                                                                                                                              Score 291; DB 14;
Pred. No. 7e-28;
1; Mismatches 1,
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                                                                                                                                B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Vanwassenaar
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                                                                                                                                                                                                                              1;
                                                                                                                                                                                                                                                  Length 57
                                                                                                                                                                                                                               Indels
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RESULT 9
AAY06670
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Best Local S
Matches 55
                                                                                                                                                                                                                                                                                                                                                                                                   The isolated bactriocin obtained from the polypeptide precursor has an inhibitory activity against selected Gram positive bacteria. The amount of bacteriocin required to provide inhibition is 15-100 arbitrary units per gram of material. The materials being treated with the bacteriocin to provide inhibition are especially foodstuff (Updated on 25-MAR-2003 to correct Pf field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Key
Protein
                                                                                                                                                                                                                                                 AAY06670 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Isolated and purified polypeptide from Lactococcus lactis sub species lactis - has inhibitory activity against gram-positive bacteria for e.g. food etc.
        Flanagan AJ,
                                                                                                26-AUG-1999
                                                                                                                                                                   Nisin Z;
                                                                                                                                                                                       Nisin Z of Lactobacillus lactis.
                                                                                                                                                                                                           09-NOV-1999
                                                                                                                                                                                                                              AAY06670;
                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Column 17-18; 13pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Henderson JT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUL-1991;
14-MAY-1992;
                                                         18-FEB-1998;
                                                                             12-FEB-1999;
                                                                                                                    WO9941978-A1
                                                                                                                                       Lactobacillus
                                                                                                                                                          feed conversion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14-MAY-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27-JUL-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US5231165-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (UNIL ) QUEST
                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1993-249768/31.
                                                                                                                                                                                                                                                                                                                                           55
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                            PFIZER
PFIZER
                                                                                                                                                                                                                                                                                                             MSTKDFNLDLVSVSKKDSGASPRITSTSLCTPGCKTGALMGCNMKTATCHCSIHVSK 57
                                                                                                                                                                   nis Z;
                                                                                                                                                                                                                                                                                                   MSTKDFNLDLVSVSKKDSGASPRITSISLCTPGCKTGALMGCNMKTATCNCSIHVSK 57
                                                                                                                                                                                                                                                                                                                                                                                  57
                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                 A,
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        Haxell
                            INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Marugg
                                                          98GB-0003424
                                                                             99WO-IB00250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 91US-0721774.
92US-0882715.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92US-0882715
                                                                                                                                                                  lantibiotic; animal performance;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24..57
/label= Bacteriocin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                         bacteriocin; probiotic
                                                                                                                                                                                                                                                Protein; 57
                                                                                                                                                                                                                                                                                                                                                   95.7%;
        ₹,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'n,
        Rolph TP;
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                                                                                                                                                                                                                                                                                                                                         Score 291; DB 14;
Pred. No. 7e-28;
1; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                            Length
                                                                                                                                                                  growth
                                                                                                                                                                                                                                                                                                                                          Indels
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RESULT 10
AAR62635
ID AAR62
XX
AC AAR62
XX
DT 15-JI
XX
DE Putal
XX
Lant
KW Lant
KW Lant
KW JP0(
XX
PN JP0(
XX
PD 13-J
XX
PF 09-
XX
XX
DR WP
XX
XX
DR WP
XX
XX
CC TT
CC TT
CC 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   relates to methods of enhancing performance in an animal by administering a bacterium capable of expressing a performance enhancing polypeptide such as nisin A or nisin Z. The enhanced performance results in improved growth rates and feed conversion efficiencies. The bacterium, which may be genetically modified to express the performance enhancing polypeptide, is administered to the gastrointestinal tract, especially to an embryo or meonatal animal. If the polypeptide is nisin, it may also inhibit ruminal methane, decrease acetate to propionate ratios and prevent amino acid deamination. Administration of an appropriate bacterium which may act as a probiotic may also help control enteric pathogens in poultry. The polypeptide is produced continuously in the gut, leaving no certified in the mean. The protein is eventually degraded,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                               Prepn. of lanthionine contg. peptide(s) antiviral drugs, immunosuppressants and
                                                                                                                                                                                                                          09-MAR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR62635
                                                                                Example
                                                                                                                                                                                                                                                          09-MAR-1993;
                                                                                                                                                                                                                                                                                           13-SEP-1994.
                                                                                                                                                                                                                                                                                                                        JP06253885-A
                                                                                                                                                                                                                                                                                                                                                        Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Putative intermediate for lanthionine-contg. peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR62635 standard; peptide; 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This sequence represents the nisin Z peptide of Lactobacillus lactis strain 22186. Nisin Z is a natural analogue of nisin A AAY06665), a lanthionine-containing bacteriocin. The invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 71; 79pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel performance enhancing method resulting in improved growth rates and feed conversion efficiencies in animals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB;
                                                                                                                                                                                            (AJIN ) AJINOMOTO KK.
                                                                                                                                                                                                                                                                                                                                                                                       Lanthionine; methyllanthionine; liimmunosuppressant; antimicrobial;
                                                                                                                                                                                                                                                                                                                                                                                      immunosuppressant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1999-527402/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MSTKDENLDLVSVSKKDSGASPRITSTSLCTPGCKTGALMGCNMKTATCHCSIHVSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   55.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 no residues in the meat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAX87793.
                                                                              2; Page 7; 8pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MSTKDFNLDLVSVSKKDSGASPRITSISLCTPGCKTGALMGCNMKTATCNCSIHVSK
                                                                                                              drugs, immunosuppressants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 57 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                            93JP-0048385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 291; DB 2
Pred. No. 7e-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ₹
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                      lantibiotic;
                                                                                                                                                                                                                                                                                                                                                                                         enzyme

    useful as antimicrobial,

                                                                                                              enzyme inhibitors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   57;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       57
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This is one of 5 peptides (AAR62635-R63639) containing Cys and Thr residues which were synthesised and tested for their useful as intermediates for the preparation of peptides which include lanthionine. Peptides 3 and 4 (AAR62637-8) produced lanthionine

produced lanthionine,

Ser or

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ITSISLCTPGCKTGALMGCNMKTATCHCSIHVSK 34

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Best Local S
Matches 33
                                      Matches
                                                                Query Match
                                                                                                               AAW66393 to AAW66469 represent native cationic peptides from the present invention. The present invention describes compositions and methods for treating infection, especially bacterial infections. The compositions and methods use cationic peptides in combination with an antibiotic agent which are then administered to a patient to enhance the activity of the antibiotic agent, to overcome: (a) tolerance; (b) acquired resistance; and (c) inherent resistance. The combinations of antibiotics and cationic peptides can provide synergistic activity against a microorganism that is tolerant, inherently resistant, or has acquired resistance to an antibiotic agent. They can be used for killing e.g. bacteria, fungi, parasites and viruses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  both lanthionine and methyllanthionine could be produced from peptide 2 (AAR62636).
                                                                                          Sequence
                                                                                                                                                                                                                                                                                                       New indolicidin peptide analogues - useful for, e.g. enhancing activity of antibiotic or overcoming tolerance, acquired resistance or inherent resistance of microorganisms
                                                                                                                                                                                                                                                                                                                                                                                       Fraser JR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-SEP-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9840401-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cationic peptide nisin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW66443;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                Disclosure; Page 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                           26-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         10-MAR-1997;
20-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lactococcus lactis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               bacteria; fungus; parasite; virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indolicidin analogue; resistance; cationic peptide; antibiotic; bacterial infection; tolerance; antibacterial; microorganism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW66443 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                 (MICR-) MICROLOGIX BIOTECH INC
                                                     Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24 ITSTSLCTPGCKTGALMGCNMKTATCHCSIHVSK 57
               24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       33;
                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
ITSTSLCTPGCKTGALMGCNMKTATCHCSIHVSK 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ITSISLCTPGCKTGALMGCNMKTATCHCSIHVSK 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34 AA;
                                                                                            34 AA;
                                                                                                                                                                                                                                                                                                                                                                                       McNicol PJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                     98US-0030619.
97US-0040649.
97US-0915314.
                                                                                                                                                                                                                                                                                                                                                                                                                                           97US-0060099.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                peptide;
                                                    60.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97.1%;
                                                                                                                                                                                                                                                                              105pp;
                                                                                                                                                                                                                                                                                                                                                                                        West MHP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34
                                                                                                                                                                                                                                                                                English.
                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 185;
Pred. No. 2
                                                     Score 185; DB 19
Pred. No. 2.8e-15
                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 15;
.8e-15;
                                                                Length 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
                                       Indels
                                      0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
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                                       Gaps
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RESULT 12
AAV91742
ID AAV91
AC AAV91
AC AAV91
XX AV91
XX Catio
XX Catio
XX Catio
XX Catio
XX Isukas
KW breas
KW breas
KW multi
XX Wo996
XX Unide
XX Unide
XX WO996
XX VA CATIO
XX WO996
XX I2-UI
XX I2-UI
XX WO996
XX WO996
XX WO996
XX WO996
XX WO996
XX I2-UI
XX II-UI
  RESULT 13
AAU90978
ID AAU90
XX
AC AAU90
XX
DT 05-JU
XX
Trans
XX
Trans
KW Ccell
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Best Local S
Matches 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This sequence represents a cationic peptide amino acid sequence, which can be used in the pharmaceutical composition of the invention. The invention relates to a pharmaceutical composition containing at least one activated polyoxyalkylene (APO)-modified cationic peptide. The modification of peptides with APO increases their activity against tumour cells, including those with a multidrug resistant phenotype. The pharmaceutical composition can be used to treat tumours; specifically lymphoma, leukaemia, multiple myeloma, or tumours of breast, lung, ovary, cervix, uterus, skin, prostate, liver and colon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cationic peptide; tumour; pharmaceutical composition; cancer; treatment; leukaemia; polyoxyalkylene-modified; APO; lymphoma; multiple myeloma; breast; lung; ovary; cervix; uterus; skin; prostate; liver; colon; multidrug resistance.
Transplant; antimicrobial peptide; pore forming agent; cell surface receptor binding compound; kidney transplant;
                                                                                                                                               05-JUN-2002
                                                                                                                                                                                                       AAU90978;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel pharmaceutical composition containing optionally polyoxyalkylene-modified cationic peptides, useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-223549/19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unidentified.
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                                                                                    Transplant media associated antimicrobial peptide #14.
                                                                                                                                                                                                                                                           AAU90978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 11; 94pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Friedland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-DEC-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (MICR-) MICROLOGIX BIOTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                             24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33
;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                           standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                     | ITSTSLCTPGCKTGALMGCNMKTATCHCSIHVSK 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 standard; Peptide; 34
                                                                                                                                                                                                                                                                                                                                                                                                     ITSISLCTPGCKTGALMGCNMKTATCHCSIHVSK 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ħ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                               (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Krieger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98US-0096541.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99WO-CA00552.
                                                                                                                                                                                                                                                           Peptide;
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                                                                                                                                               entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IJ,
                                                                                                                                                                                                                                                              34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 185; DB 21;
Pred. No. 2.8e-15;
0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Taylor R,
                                                                                                                                                                                                                                                           A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 34;
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treating tumours
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Charles to waster of many few

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RESULT 14
ABU59619
ID ABU59
XX ABU59
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XX Catic
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XX Targe
KW Targe
KW Cathe
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KW Cathe
KW Cathe
XX Cathe
XX Synth
XX Synth
XX Synth
US2002041898-A1
                                     tumour; cationic
                                     cancer-targeting peptide.
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22-APR-2003 ABU59619 밁

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24 \_

Matches Query Match

Local

l Similarity 33; Conserv

Sequence

₩ 4

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The invention describes new transplant compositions comprising CC antinicrobial polypeptides or pore forming agents and/or cell surface receptor binding compounds. The media is capable of extending the present period past 72 hours and can provide organs with increased functionality upon transplant. animals receiving kidneys stored in the case control animals receiving kidneys stored in the creation levels of less than half of those observed in control animals receiving kidneys stored in UW solution (defined in the specification) creatinine levels are indicative of healthier kidneys and amore preferable prognosis for the transplant patient. The media of the invention are useful for decreasing the incidence and/or severity of delayed graft function in patients receiving transplanted kidneys stored and/or treated in the media. The media may also be used in procedures such as cardioplegia. It is contemplated that transplant of healthier creams leads to a decrease in chronic rejection. This sequence represents and an animalicrobial peptide studied in the development of the transplant
                                                                                                  Targeting ligand; bioactive agent; polymer matrix; cancer; cytostatic; cathepsin-D substrate; peptides; neuroreceptor; adrenal receptor; fibronectin; vitronectin; integrin; RGD motif; angiogenic endothelium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Media comprising antimicrobial polypeptides or pore forming agents and/or cell surface receptor binding compounds useful for the storage and preservation of organs prior to transplant -
                                                                                                                                                                                      Cationic cancer -targeting peptide #51.
                                                                                                                                                                                                                                                                                                                 ABU59619 standard; Peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 25; 78pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27-JUL-2001; 2001WO-US23785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cardioplegia; organ transplant; transplant rejection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 | ITSTSLCTPGCKTGALMGCNMKTATCHCSIHVSK
                                                                                                                                                                                                                                                                                                                                                                                                                             ITSISLCTPGCKTGALMGCNMKTATCHCSIHVSK 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60.9%;
nilarity 97.1%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; 2000US-221632P.
; 2000US-249602P.
; 2001US-290932P.
                                                                                                                                                                                                                                (first entry)
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                                                                                                                                                                                                                                                                                                                   34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 185; DB 23; Pred. No. 2.8e-15; O. Mismatches 1;
                                                                                                                                                                                                                                                                                                                   B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
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AAY31659
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a composition comprising a bioactive agent chomogeneously dispersed in a targeted matrix (polymer and targeting ligand). Also included are a targeted matrix for use as a delivery vehicle comprising a polymer associated with a targeting ligand, cenhancing the bioavailability of an agent comprising administration of the composition and treating cancer comprising administration of the novel composition and treating to targeting ligand may be a peptide especially in cancer therapy. The targeting ligand may be a peptide especially in cancer therapy. The targeting ligand may be a peptide substrate peptides, peptides are disclosed including cathepsin. It is the peptides recognising fibronectin and vitronectin-binding integrins, peptides targeting the RGD (Arg-Gly-Asp)-motif in, e.g., antibodies, peptides targeting the RGD (Arg-Gly-Asp)-motif in, e.g., integrins, peptides targeting the RGD (Arg-Gly-Asp)-motif in, e.g., antibodies, tissue specific peptides (e.g. of lung, skin, pancreas, instance, uterus, adrenal gland and retina), and cationic cancertargeting peptides. The present sequence is a peptide targeting cligand disclosed in the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local (
                                                                                                                        Chimeric
Chimeric
                                                                                                                                                                                                                                                    Subtilin-nisin chimera.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Targeted delivery system dispersed in a targeted \pi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unger EC,
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31-OCT-2000;
                   Protein
                                                                                                                                                                                        preservative.
                                                                                                                                                                                                              Nisin;
                                                                                                                                                                                                                                                                                             09-NOV-1999
                                                                                                                                                                                                                                                                                                                                       AAY31659;
                                                                                                                                                                                                                                                                                                                                                                                 AAY31659 standard; Protein; 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page14; 46pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2003-208921/20.
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                                                           Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (UNGE/) UNGER E C.
(MATS/) MATSUNAGA T O.
(RAMA/) RAMASWAMI V.
(ROMA/) ROMANOWSKI M J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24 ITSTSLCTPGCKTGALMGCNMKTATCHCSIHVSK 57
                                                                                                                                                                                                        subtilin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ITSISLCTPGCKTGALMGCNMKTATCHCSIHVSK 34
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                                                                                                                        Lactococcus lactis. Bacillus subtilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34 AA;
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2000US-0703474.
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                                                                                                                                                                                                                                                                                           (first entry)
                   /note= "signal peptide"
8..41
                                                                            Location/Qualifiers
/note= "mature protein"
                                                                                                                                                                                                            lantibiotic; chimera; mutant; bacteriocide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    m comprising a bioactive agent homogeneously matrix is especially useful in cancer therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ramaswami V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 185; DB 24;
Pred. No. 2.8e-15;
0; Mismatches 1,
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drug, the

Gaps

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28-JUL-2000; 17-NOV-2000; 15-MAY-2001;

07-FEB-2002

Lactococcus lactis.

Murphy CJ,

Reid TW,

(MURP/) MURPHY C J.

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Search completed: January 12, 2004, 14:24:21 Job time : 49 secs
                                                                                                                                                                                                                                                                                                                                                                                         The present sequence represents a chimeric pre-peptide composed of a subtilin leader region and a subtilin-nisin fusion comprising residues 1-11 of Bacillus subtilis subtilin and residues 12-32 of Lactococcus lactis nisin. The subtilin-nisin fusion was not processed into a functional lantiblotic when expressed in B. subtilis. A heterogeneous mixture of products was produced, with none of the products having the expected properties of a correctly processed polypeptide. However, the mixture contained a minor component with a specific activity that exceeded that of nisin. The invention provides lantiblotic mutants and chimeras (see also AAV31658) having enhanced activity and stability compared to nisin and subtilin. They can be produced by cultivation of transformed host cells and used e.g. as food preservatives to treat, kill or inhibit the growth of microorganisms and/or their spores.
                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 33; Conserv
                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lantibiotic mutants and chimera(s) - having enhanced stability and activity compared to nisin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-SEP-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example; Fig 2; 60pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1997-225847/20.
N-PSDB; AAX87829.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hansen JN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-SEP-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      03-APR-1997.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Region
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                                                                                                                  41 AA;
                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95US-0535494.
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/note= "nisin (1-11)"
19..41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "subtilin(12-32)"
                                                                                                                                                                                                                                 59.5%; Score 181; DB 18; Length 41; 80.5%; Pred. No. 1.1e-14; tive 2; Mismatches 6; Indels
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Result
No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Post-processing: Minimum Match 0%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OM protein - protein search, using sw model
  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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 285
282.5
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291
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seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                        Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  328717 seqs, 42310858 residues
                                                                                                                                                                                                                                                                                                                                                                                    Query
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Issued_Patents_AA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MSTKDFNLDLVSVSKKDSGA.....ALMGCNMKTATCHCSIHVSK 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Copyright
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/backfiles1.pep:*
                                                                                                                                                                                                                                                                                                                                                                     Length
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US-08-315-579-2
US-08-836-687B-40
US-08-836-687B-42
US-08-836-687B-42
US-08-836-687B-44
US-08-836-687B-44
US-08-836-687B-45
US-08-773-731A-2
US-08-836-687B-41
US-08-836-687B-47
            US-08-535-494-9

US-09-097-635-9

US-07-880-003-11-2

US-08-030-911-1

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US-07-981-525-7

US-07-981-525-7

US-07-981-525-7
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US-08-836-687B-26
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US-09-462-478A-8
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42, Appl
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US-08-836-687B-51	US-08-836-687B-50	US-08-836-687B-49	US-08-986-617-25	80-	US-08-524-677-10	US-09-097-635-5	-08-535-494-	-08-986-617-	US-08-465-491-9	US-08-220-033-9	US-07-981-525-9	US-09-462-478A-9	US-09-030-619-208	-08-986-617	US-08-986-617-2	US-08-465-491-7	US-08-465-491-2	
Sequence 51, Appl	Sequence 50, Appl	•	Sequence 25, Appl	-	Sequence 10, Appl	Sequence 5, Appli	Sequence 5, Appli		-	•	-	Sequence 9, Appli	208	-	•	•	Sequence 2, Appli	

## ALIGNMENTS

US-08-836-687B-20

GENERAL INFORMATION:

Sequence 20, Application US/08836687B Patent No. 6448034

APPLICANT: Gasson, Michael John
APPLICANT: Dodd, Helen Mair
TITLE OF INVENTION: PRODUCTION OF VARIANT NISIN
FILE REFERENCE: 2014/7/70
CURRENT APPLICATION NUMBER: US/08/836,687B
CURRENT FILING DATE: 1995-11-20
NUMBER OF SEQ ID NOS: 51
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 20

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LENGTH: 57
; TYPE: PRT
; ORGANISM: Lactococcus
US-08-836-687B-20
                                                                                   SOFTWARE: Par
; SEQ ID NO 8
; SEQ THE ST
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US-09-462-478A-8
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                                                                                                                                                                                                                                                                                 Sequence 8, Application US/09462478A Patent No. 6541607
GENERAL INFORMATION:
           IENGTH: 57
TYPE: PRT
ORGANISM: Unknown
PEATURE:
PEATURE INFORMATION: Nisin A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/462,478A CURRENT FILING DATE: 2000-04-17 PRIOR APPLICATION NUMBER: US/60/053,035 PRIOR FILING DATE: 1997-07-18 NUMBER OF SEQ ID NOS: 18
                                                                                                                                                                                                                                 TITLE OF INVENTION: SUBLANCIN LANTIBIOTIC PRODUCED BY BACILLUS SUBTILIS FILE REFERENCE: 8172-8072
                                                                                                                                                                                                                                                                  APPLICANT: UNIVERSITY OF MARYLAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      56;
                                                                                                                        PatentIn Ver.
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98.2%;
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Pred. No. 1.8e-29;
0; Mismatches 1
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US-08-836-687B-28
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US-08-836-6878-24
                                                  Sequence 28, Application US/08836687B Patent No. 6448034 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: PRODUCTION OF VARIANT NISIN FILE REFERENCE: 20747/70
CURRENT APPLICATION NUMBER: US/08/836,687B
CURRENT FILING DATE: 1995-11-20
NUMBER OF SEQ ID NOS: 51
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: 20747/70
CURRENT APPLICATION NUMBER: US/08/836,687B
CURRENT FILING DATE: 1995-11-20
NUMBER OF SEQ ID NOS: 51
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 24
LENGTH: 57
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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APPLICANT: Gasson, Michael Jo
APPLICANT: Dodd, Helen Mair
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APPLICANT: Gasson, Michael John
APPLICANT: Dodd, Helen Mair
TITLE OF INVENTION: PRODUCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -08-836-6878-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Gasson, Michael John
APPLICANT: Dodd, Helen Mair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: PRODUCTION OF VARIANT NISIN
                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Lactococcus sp.
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ORGANISM: Lactococcus sp
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 PRODUCTION OF VARIANT NISIN
                                                                                                                                                                                                                                                            97.0%;
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96.5%;
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                                                                                                                                                                                                                                              Score 295; DB 4; Length 57; Pred. No. 4.1e-29; Indels
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Pred. No. 4.1e-29;
1; Mismatches 1
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Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                          APPLICATION NUMBER: NL 9100634
FILING DATE: 11-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/NL92/00068
FILING DATE: 09-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: PATCH, ANDIEN: 32,925
REGISTRATION NUMBER: 32,925
REFERENCE/DOCKET NUMBER: BO 37078
                                                                                                                                        TELEFAX: 703/685-0573
TELEX: 248425 EMBON
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/08/836,687B
CURRENT FILING DATE: 1995-11-20
NUMBER OF SEQ ID NOS: 51
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 57
TYPE: PRT
ORGANISM: Lactococcus sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: ITITLE OF INVENTION: ITITLE OF INVENTION: ITITLE OF INVENTION: NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR TON NUMBER: NL 9100634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0,
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
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                                                                    TOPOLOGY: 1:
DLECULE TYPE:
                                                                                                                                                                                TELEPHONE: /UJ/ -- TELEPHONE: /UJ/ -- 703/685-0573
                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/0 FILING DATE: 07-OCT-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: UZIP: 22202
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                                                                                                                       LENGTH:
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                                                                                                     amino acid
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                                                                                                                       57 amino acids
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745 South 23rd Street, Second Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KUIPERS,
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94.7%;
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95.7%;
96.5%;
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ACID BACTERIA WHICH PRODUCE SUCH LANTIBIOTICS, METHOD
CONSTRUCTING SUCH LACTIC ACID BACTERIA AND METHOD FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRESERVING FOODSTUFFS WITH ETC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Release #1.0,
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Pred. No. 9.6e-29;
Score 291; DB 1;
Pred. No. 1.3e-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 57;
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RESULT 8
US-08-836-687B-40
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                                                                                                                                                Query Match 95.7%;
Best Local Similarity 96.5%;
Matches 55; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 08/129,151
FILING DATE: 07-OCT-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: NL 9100634
FILING DATE: 11-APR-1991
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                        TELEX: 248425 EMBON INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
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LENGTH: 57 amino acids
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/715,579
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TELEPHONE: 703/521-2297
TELEFAX: 703/685-0573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: PCT/I
FILING DATE: 09-APR-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                          MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: PATCH, Andrew J.
REGISTRATION NUMBER: 32,925
REFERENCE/DOCKET NUMBER: BO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/01
FILING DATE: 19-SEP-1996
                                                                                                                                                                                                                                                                TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 22202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Arlington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3: c/o YOUNG & THOMPSON
745 South 23rd Street, Second Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
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                                                                                                                                                                                                                                                                linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PCT/NL92/00068
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                                                                                                                                                                  Score 291; DB 2;
Pred. No. 1.3e-28;
                                                                                                                                              Mismatches
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FILE REFERENCE: 20747/00
CURRENT APPLICATION NUMBER: US/08/836,687B
CURRENT FILING DATE: 1995-11-20
NUMBER OF SEQ ID NOS: 51
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 43
LENGTH: 57
TYPE: PRT
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US-08-836-687B-43
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                                                TITLE OF INVENTION: PRODUCTION OF VARIANT NISIN FILE REFERENCE: 20747/70 CURRENT APPLICATION NUMBER: US/08/836,687B CURRENT FILING DATE: 1995-11-20 NUMBER OF SEQ ID NOS: 51 SOFTWARE: Patentin Ver. 2.1 SEQ ID NO 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 43, Application US/08836687B Patent No. 6448034 GENERAL INFORMATION:
                                                                                                                                                                                                                Patent No. 6448034
GENERAL INFORMATION:
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CURRENT APPLICATION NUMBER: US/08/836,687B
CURRENT FILING DATE: 1995-11-20
NUMBER OF SEQ ID NOS: 51
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 40
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                                                                                                                                                                                                                                                       Sequence 42,
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APPLICANT: Dodd, Helen Mair
TITLE OF INVENTION: PRODUCTION OF VARIANT NISIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT Gasson, Michael John
APPLICANT: Dodd, Helen Mair
TITLE OF INVENTION: PRODUCTION OF VARIANT NISIN
                                                                                                                                                                              APPLICANT: Gasson, Michael John APPLICANT: Dodd, Helen Mair
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ORGANISM: Lactococcus sp
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                      TYPE: PRT
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Pred. No. 1.3e-28;
0; Mismatches 2
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Pred. No. 1.3e-28;
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Query Match

DB 4; Length 57

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RESULT 13
US-08-836-687B-45
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US-08-836-687B-44
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US-08-836-687B-46
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Sequence 45, Application US/08836687B
Patent No. 6448034
GENERAL INFORMATION:
APPLICANT: Gasson, Michael John
APPLICANT: Dodd, Helen Mair
TITLE OF INVENTION: PRODUCTION OF VARIANT NISIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: PRODUCTION OF VARIANT NISIN FILE REFERENCE: 20747/70
CURRENT APPLICATION NUMBER: US/08/836,687B
CURRENT FILING DATE: 1995-11-20
NUMBER OF SEQ ID NOS: 51
SOPTWARE: Patentin Ver. 2.1
SEQ ID NO 46
LENGTH: 57
                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Ver. 2.1 SEQ ID NO 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 44, Application Patent No. 6448034 GENERAL INFORMATION:
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APPLICANT: Gasson, Michael John
APPLICANT: Dodd, Helen Mair
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Best Local
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APPLICANT: Dodd, Helen Mair
TITLE OF INVENTION: PRODUCTION OF VARIANT NISIN
FILE REFERENCE: 20747/70
CURRENT APPLICATION NUMBER: US/08/836,687B
CURRENT FILING DATE: 1995-11-20
NUMBER OF SEQ ID NOS: 51
                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Lactococcus sp
                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
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Pred. No. 2.2e
0; Mismatches
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Pred. No. 2.2e-28;
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RESULT 14
US-08-773-731A-2
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CURRENT APPLICATION NUMBER: US/08/836,687B
CURRENT FILING DATE: 1995-11-20
NUMBER OF SEQ ID NOS: 51
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/08773731A Patent No. 6100056
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                                Query Match
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                                                                                                                                                    TELEFAX: 202-887-0689
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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TYPE: PRT
ORGANISM: Lactococcus sp.
                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: GB 9207267.7 FILING DATE: 02-APR-1992 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08
FILING DATE: 18-NOV-1994
PRIOR APPLICATION DATA:
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                                                                                      MOLECULE TYPE:
                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: NISINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Gasson, Michael J
APPLICANT: Dodd, Helen M.
                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                          NAME: Brady, Jr., James W.
REGISTRATION NUMBER: 32,115
REFERENCE/DOCKET NUMBER: E8280.016/P016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Match 93.8%;
Local Similarity 94.7%;
                                                                                                     TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: PCT/
FILING DATE: 01-APR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                       LENGTH: 83 amino acids
                                                                                                                                                                                                          TELEPHONE:
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                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MSTKDFNLDLVSVSKKDSGASPRITSTSLCTPGCKTGALMGCNMKTATCHCSIHVSK 57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                                                                                   protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Floppy disk
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                93.8%;
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                                                                                                                                                                                                                                                                                                                                                                                    PCT/GB93/00676
                                                                                                                                                                         2
Score 285; .DB 3; Length 83; Pred. No. 1e-27; O; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 285; DB 4;
Pred. No. 6.8e-28;
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Result
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Scoring table:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Run on:
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                                                                                                                                                                                                                                                                                                                                            Score
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1: /cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*

7: /cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*

8: /cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*
                                                                                                                                                                                                                                                                                                                                            Match
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Listing first 45 summaries
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Copyright (c) 1993 - 2004 Compugen Ltd.
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/cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
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US-09-917-340-14
2 US-10-277-233-206
US-09-030-619-208
               US-10-372-098-9
US-10-082-618-4
US-10-277-233-208
US-10-372-098-10
US-10-082-618-6
US-10-082-618-1
US-10-184-634-211
US-10-184-634-211
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0-184-644-211
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0-140-472-67
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               Sequence 206, App
Sequence 14, Appl
Sequence 208, App
Sequence 208, App
Sequence 9, Appli
Sequence 4, Appli
Sequence 10, Appl
Sequence 10, Appl
Sequence 1, Appl
Sequence 1, Appl
Sequence 211, App
Sequence 211, App
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15	12	16	15	12	12	12	12	12	12	12	12	12	12	15	15	12	75	75	16	15	12	12	12	12	12	12	12	12	12
US-10-184-644-147	-10-063-685-3	-10-146-731-31	-10-123-155-31	0-141-759-	-10-141-756-31	-10-140-923-31	-10-140-864-31	0-140-805-	-10-137-871-31	-10-158-790-31	-10-142-885-31	-761-31	-10-140-472-31	-10-184-634-23	-10-184-644-23	-10-063-685-6	-10-184-634-3	-10-184-644-33	-10-146-731-6	-10-123-155-	-10-141-759-6	-10-141-756-6	0-140-923-	-10-140-864-	- 50	0-137-871-	58-790-6	-10-142-885-	US-10-141-761-67
e 147	Sequence 31, Appl	equence 317	e 317	e 317	e 317,	e 317,	e 317,	e 317,	equence 317,	e 317,	e 317,	e 317,	e 317,	equence 235,	equence 235,	e 61,	equence 335,	e 335,	equence 67,	equence 67,	equence 67,	equence 67,	e 67,	e 67,	e 67,	e 67,	equence 67,	equence	

## ALIGNMENTS

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RESULT 2
US-10-372-098-8
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US-10-082-618-5
Sequence 8, Application US/10372098
Publication No. US20030166835A1
GENERAL INFORMATION:
APPLICANT: UNIVERSITY OF MARYLAND
TITLE OF INVENTION: SUBLANCIN LANTIBIOTIC PRODUCED BY BACILLUS SUBTILIS 168
FILE REFERENCE: 8172-8072
CURRENT APPLICATION NUMBER: US/10/372,098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/10/082,618
CURRENT FILING DATE: 2002-02-22
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 5
LENGTH: 57
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 5, Application US/10082618 Publication No. US20030175207A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: OLSTEIN, ALAN D.
APPLICANT: FEIRTAG, JOELLEN
TITLE OF INVENTION: BACTERIOCIN-METAL COMPLEXES IN THE DETECTION OF
TITLE OF INVENTION: BATHOGENS AND OTHER BIOLOGICAL ANALYTES
FILE REFERENCE: 7005-0003
                                                                                                                                                                                                                                                                                                                                                             Local
                                                                                                                                                                                                                                                  ch 100.0%; Score 304; DB 12; Similarity 100.0%; Pred. No. 2.5e-29; S7; Conservative 0; Mismatches 0;
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Sequence 14, Application US/09917340
Patent No. US20020090369A1
GENERAL INFORMATION:
APPLICANT: Murphy, Christopher J.
APPLICANT: McAnulty, Jonathan F.
APPLICANT: Reid, Ted W.
TITLE OF INVENTION: Transplant Media
PILE REFERENCE: TPLANT-06468
CURRENT APPLICATION NUMBER: US/09/917,340
CURRENT FILING DATE: 2001-07-29
PRIOR APPLICATION NUMBER: 60/221,632
PRIOR FILING DATE: 2000-07-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT FILING DATE: 2003-02-25
PRIOR APPLICATION NUMBER: US/09/462,478A
PRIOR FILING DATE: 2000-04-17
PRIOR APPLICATION NUMBER: US/60/053,035
PRIOR FILING DATE: 1997-07-18
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PATENTIN VET. 2.0
SEQ ID NO 8
LENGTH: S7
TYPE: PRT
ORGANISM: Unknown
PERTURE: 1997-07-18
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US-09-917-340-14
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US-09-030-619-206
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Fraser, Janet R.
APPLICANT: West, Michael H.P.
APPLICANT: MCNicol, Patricia J.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
TITLE OF INVENTION: INPECTIONS USING CATIONIC PEPTIDES ALONE OR
TITLE OF INVENTION: WITH ANTIBIOTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE: 660081.406
CURRENT APPLICATION NUMBER: US/09/030,619B
CURRENT FILLING DATE: 1998-02-25
NUMBER OF SEQ ID NOS: 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FastSEQ for Windows Version 3.0
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Erfle, Douglas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Krieger, Timothy J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Application US/09030619B
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Pred. No. 2.
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Pred. No. 1.3e-28;
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.8e-15;
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; TYPE: PRT
; ORGANISM: Lactococcus lactis
US-09-917-340-14
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 206
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SEQ ID NO 14
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Best Local Similarity
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APPLICANT: MCNÍCO1, PATRÍCIA J.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
TITLE OF INVENTION: INFECTIONS USING CATIONIC PEPTIDES ALC
TITLE OF INVENTION: WITH ANTIBIOTICS
FILE REFERENCE: 660081.406
CURRENT APPLICATION NUMBER: US/09/030,619B
CURRENT FILLING DATE: 198-02-25
NUMBER OF SEQ ID NOS: 232
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Fraser, Janet R.
APPLICANT: West, Michael H.P.
APPLICANT: McNicol, Patricia J.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATIN
TITLE OF INVENTION: INFECTIONS USING CATIONIC PEPTIDES
TITLE OF INVENTION: MITH ANTIBIOTICS
FILE REFERENCE: 660081.406C1
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PRIOR FILING DATE: 2001-05-15
NUMBER OF SEQ ID NOS: 96
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CURRENT FILING DATE: 2002-10-18
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TYPE: PRT
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Local Similarity 97.1%;
nes 33; Conservation
                                                                                                                                                                                                                                                                                       208, Application US/09030619B
5. US20020035061A1
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                                                                                                                                                                      Fraser, Janet R. West, Michael H.P.
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Erfle, Douglas
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97.1%;
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Pred. No. 2.8e-15;
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Pred. No. 2.8e-15;
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TITLE OF INVENTION: BACTERIOCIN-METAL COMPLEXES IN THE DETECTION (
TITLE OF INVENTION: BACTERIOCIN-METAL COMPLEXES IN THE DETECTION (
FILE REFERENCE: 7005-0003
CURRENT APPLICATION UMBER: US/10/082,618
CURRENT FILING DATE: 2002-02-22
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 4
LENGTH. 6.
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CURRENT FILING DATE: 2003-02-25
PRIOR APPLICATION NUMBER: US/09/462,478A
PRIOR FILING DATE: 2000-04-17
PRIOR APPLICATION NUMBER: US/60/053,035
PRIOR FILING DATE: 1997-07-18
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 9
LENGTH: 56
TYPE: PRT
ORGANISM: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; FEATURE:
; OTHER INFORMATION: subtilin
US-10-372-098-9
                                                                                                   ; TYPE: PRT ; ORGANISM: Bacillus subtilis US-10-082-618-4
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; TYPE: PRT
; ORGANISM: Bacillus subtilis
US-09-030-619-208
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Publication No. US20030166835A1
GENERAL INFORMATION:
                                                  Query Match
Best Local Similarity
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                                    Matches
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Best Local Similarity
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TITLE OF INVENTION: SUBLANCIN LANTIBIOTIC PRODUCED BY BACILLUS SUBTILIS 168
FILE REFERENCE: 8172-8072
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DFNLDLVSVSKKDSGASPRITSTSLCTPGCKTGALMGCNMKTATCHCSI 53
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nilarity 59.2%;
Conservative
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                                                Score 157; DB 12;
Pred. No. 1.1e-11;
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Pred. No. 1.1e-11;
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                                  Mismatches
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US-10-372-098-10
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LENGTH: 52
TYPE: PRT
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
TITLE OF INVENTION: INFECTIONS USING CATIONIC PEPTIDES ALONE OR IN COMBINATION
TITLE OF INVENTION: WITH ANTIBIOTICS
FILE REFERENCE: 660081.406C1
CURRENT APPLICATION NUMBER: US/10/277,233
CURRENT FILING DATE: 2002-10-18
NUMBER OF SEQ ID NOS: 232
SOFTMARE: PastSEQ for Windows Version 3.0
SEQ ID NO 208
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Best Local Similarity 59.2%;
Matches 29; Conservative
                                                                                          Matches
                                                                                                                                  Query Match
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TITLE OF INVENTION: SUBLANCIN LANTIBIOTIC PRODUCED BY BACILLUS SUBTILIS 168
FILE REFERENCE: 8172-8072
CURRENT APPLICATION NUMBER: US/10/372,098
CURRENT FILING DATE: 2003-02-25
PRIOR APPLICATION NUMBER: US/99/462,478A
PRIOR FILING DATE: 2000-04-17
PRIOR APPLICATION NUMBER: US/60/053,035
PRIOR APPLICATION NUMBER: US/60/053,035
PRIOR PILING DATE: 1997-07-18
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.0
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                                                                                                                                                                                                                             FEATURE:
                                                                                                                                                                                                                                                  ORGANISM: Unknown
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                                                                                                             Match 31.1%;
Local Similarity 62.2%;
11 FNLD-VKVNAKESNDSGAEPRIASKFICTPGCAKTGS 46
                                          6 FNLDLVSVSKK---DSGASPRITSTSLCTPGC-KTGA 38
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                                                                                          23; Conservative
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Pred. No. 1.1e-11;
8; Mismatches 12;
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                                                                                                             Score 94.5; DB 12; Length 52; Pred. No. 0.00033;
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RESULT 11 US-10-082-618-6

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US-10-082-618-1
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; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-10-082-618-6
                                                                                                                                                                                                                                                                                                                 US-10-184-644-211
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SEQ ID NO 1
LENGTH: 52
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APPLICANT: OLSTEIN, ALAN D.
APPLICANT: FEIRTAG, JOELLE
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SEQ ID NO 6
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Best Local Similarity
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CURRENT APPLICATION NUMBER: US/10/082,618
CURRENT FILING DATE: 2002-02-22
NUMBER OF SEQ ID NOS: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/10/082,618
CURRENT FILING DATE: 2002-02-22
NUMBER OF SEQ ID NOS: 8
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TITLE OF INVENTION: BACTERIOCIN-METAL COMPLEXES IN THE DETECTION OF
TITLE OF INVENTION: PATHOGENS AND OTHER BIOLOGICAL ANALYTES
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Local Similarity 62.2%;
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: Zhang, Zemin
INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
                                                                                                                             Desnoyers, Luc
Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
                                                                                                                                                                                                                                                                                                                                                                                              FDLD-VKVNAKESNDSGAEPRIASKFLCTPGCAKTGS 46
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                                                                    Smith, Victoria Watanabe, Colin K.
                                                  Wood, William I.
                                                                                                                                                                                                                                                                                              Application US/10184644
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Pred. No. 0.00076;
3; Mismatches 6
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Pred. No. 0.00033
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RESULT 15
US-10-140-472-67
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; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-184-644-211
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CURRENT APPLICATION NUMBER: US/10/184,644
CURRENT FILING DATE: 2002-06-28
Prior Application removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 612
SEQ ID NO 211
LENGTH: 708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 211, Appropriate Publication No.
                                                                                                                                                      Sequence 67, App
Publication No.
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NUMBER OF SEQ ID NOS: 612
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CURRENT FILING DATE: 2002-06-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3430R1C217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Baker, Kevin P.
                   APPLICANT:
                                    APPLICANT:
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TYPE: DNA
ORGANISM: Homo Sapien
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l Similarity 43.2%;
l6; Conservative
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                                                                                                                     Baker, Kevin P.
                                                                                    Beresini, Maureen
DeForge, Laura
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Gerritsen, Mary E. Goddard, Audrey
                                                  Desnoyers, Luc
Filvaroff, Ellen
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Goddard, Audrey
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                                   Gao, Wei-Qiang
                                                                                                                                                                    Application US/10140472
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                                                                                                                                                                                                                                                                                                                                          24.0%;
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Pred. No. 2.3;
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APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Sewart. Timothy A.
APPLICANT: Stewart. Timothy A.
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330RIC168
CURRENT APPLICATION NUMBER: US/10/140,472
CURRENT APPLICATION NUMBER: US/10/140,472
CURRENT FILING DATE: 2002-05-06
PRIOT APPLICATION REMOVED - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 67
LENGTH: 4185
TYPE: DNA
ORGANISM: Homo Sapien
US-10-140-472-67
Search completed: January 12, 2004, 14:23:23 Job time: 49 secs
                                                                                                          밁
                                                                                                                                                                                                    Query Match 23.0%; Score 70; DB 12; Length 4185; Best Local Similarity 46.4%; Pred. No. 38; Matches 13; Conservative 2; Mismatches 11; Indels 2
                                                                                                     11; Indels 2; Gaps
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GenCore version 5.1.6

Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on:

January 12, 2004, 14:22:27; Search time 26 Seconds (without alignments) 210.831 Million cell updates/sec

Title:

US-10-082-618-5

Perfect score:
304

Sequence:
1 MSTKDFNLDLVSVSKKDSGA......ALMGCNMKTATCHCSIHVSK 57

Scoring table:
BLOSUM62
Gapop 10.0, Gapext 0.5

Searched:
283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters:
283308

Minimum DB seq length:
00

Maximum Match 100%
Listing first 45 summaries

Database:
1: $\overline{\text{Dirl:*}}{\text{Dirl:*}}$
1: $\overline{\text{Dirl:*}}{\text{Dirl:*}}$
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3: $\overline{\text{Dirl:*}}{\text{3: pir4:*}}$
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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17.8	17.8	17.8	17.8	17.8	17.8	17.8	17.8	17.8	17.8	17.9	18.1	18.1	18.1	18.1	18.1
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probable rnd efflu	AcrB/AcrD/AcrF fam	unknown protein, 2	DNA topoisomerase	Tid(56) protein -	pyruvate kinase (E	protein T3P18.9 [i	ornithine cyclodea	transcription fact	transcription fact	hypothetical prote	replication licens	conserved hypothet	bud emergence medi	gas1 protein - mou	alcohol dehydrogen

ALIGNMENTS

A;Residues: 1-57 < STE> A;Cross-references: GB:M65089; NID:g149447; PIDN:AAA73038.1; PID:g149448 A;Experimental source: ATCC 11454 R;Mulders, J.W.M.; Boerrigter, I.J.; Rollema, H.S.; Siezen, R.J.; de Vos, W.M. Eur. J. Biochem. 201, 581-584, 1991 A;Title: Identification and characterization of the lantibiotic nisin Z, a natural nisin A;Title: Insulation and characterization of the lantibiotic nisin Z, a natural nisin A;Reference number: S17858; MUID:92037612; pMID:1935953 A;Accession: S17858 A;Accession: S17858 A;Molecule type: DNA A;Residues: 1-49,'N',51-57 <mul> A;Cross-references: EMBL:X61144; NID:944046; PIDN:CAA43440.1; PID:944047 A;Experimental source: strain NIZO 22186 A;Note: nisin Z allelic variant; amino acid composition and structure determination by NN</mul>	J. Gen. Microbiol. 136, 555-566, 1990 A;Title: Analysis of the genetic determinant for production of the peptide antibiotic nis A;Reference number: A45821; MUID:90362041; PMID:2118169 A;Accession: B45821 A;Molecule type: DNA A;Residues: 1-57 < DODS A;Cross-references: GB:M27277; NID:g149440; PIDN:AAA25188.1; PID:g149441 A;Cross-references: GB:M27277; NID:g149440; PIDN:AAA25188.1; PID:g149441 A;Cross-references: GB:M27277; NID:g149440; PIDN:AAA25188.1; PID:g149441 A;Title: Characterization of the nisin gene as part of a polycistronic operon in the chrc A;Reference number: A43743; MUID:91282469; PMID:1905517 A;Accession: A43743 A;Molecule type: DNA A;Molecule type: DNA A;Molecule type: DNA	A; Molecule type: DNA A; Residues: 1-57 < BUC> A; Cross-references: GB:J04057; NID:g153816; PIDN:AAA88606.1; PID:g153817 A; Cross-references: GB:J04057; NID:g153816; PIDN:AAA88606.1; PID:g153817 A; Note: the authors identified the species as Streptococcus lactis R; Kaletta, C; Entian, K.D. J. Bacteriol. 171, 1597-1601, 1989 J. Bacteriol. 171, 1597-1601, 1989 A; Title: Nisin, a peptide antibiotic: cloning and sequencing of the nisA gene and posttration of the sequence number: A32809; MUID:89153467; PMID:2493449 A; Recession: A32809 A; Molecule type: DNA A; Residues: 1-57 < KALD A; Cross-references: GB:M24527; NID:g341189; PIDN:AAA26948.1; PID:g530218 R; Dodd, H.M.; Horn, N.; Gasson, M.J.	RESULT 1  NILLSA  NISHA precursor - Lactococcus lactis  N;Alternate names: nisin A; nisin Z  C;Species: Lactococcus lactis  C;Date: 21-May-1990 #sequence revision 12-May-1994 #text_change 18-Jun-1999  C;Accession: A31915; A32809; B45921; A43743; S17858; B48951; S36734; S70485; S16779; S365;  C;Accession: G.W.; Banerjee, S.; Hansen, J.N.  J. Biol. Chem. 263, 16260-16266, 1988  A;Title: Structure, expression, and evolution of a gene encoding the precursor of nisin,  A;Reference number: A92679; MUID:89034093; PMID:3141403  A;Accession: A31915

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subtilin precursor - Bacillus subtilis (strain ATCC 6633)
N;Alternate names: SpaS; subtilin A
N;Contains: subtilin B
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A; Accession: S70485
                                                                                                           NIBSSA
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FEBS Lett. 330, 23-27, 1993
A;Title: Biosynthesis and secretion of a precursor of nisin Z by Lactococcus lactis, A;Reference number: S36142; MUID:93380562; PMID:8370453
A;Contents: annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Experimental source: strain 6F3
A;Note: sequence extracted from NCBI backbone (NCBIN:122292, NCBIP:122295)
R;Kuipers, O.P.; Beerthuyzen, M.M.; Siezen, R.J.; de Vos, W.M.
Eur. J. Biochem. 216, 281-291, 1993
By Title: Characterization of the nisin gene cluster nisABTCIPR of Lactococcus lactis. Re
A;Raterence number: S36734; MUID:93373937; PMID:7689965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: protein
A;Residues: 24-57 <CHA>
C;Comment: Nisin is secre
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R;Gross, E.; Morell, J.L.
J. Am. Chem. Soc. 93, 4634-4635, 1971
A;Title: The structure of nisin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-57 < ENG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;Superfamily: subtilin precursor
;Keywords: antibiotic; lanthionine
;Reywords: antibiotic; lanthionine
;2-23/Domain: propeptide #status experimental <MAT>
;2-23/Domain: propeptide #status experimental <MAT>
;2-3-24/Cleavage site: Arg-Ile (proteinase Nisp) #status experimental
;2-25/Modified site: dehydrobutyrine (Thr) #status experimental
;2-26/Modified site: dehydroalanine (Ser-Cys) #status experimental
;2-28/Modified site: dehydroalanine (Ser) #status experimental
;3-28/Modified site: dehydroalanine (Ser) #status experimental
;3-31-34/Cross-link: (25,35,6R)-3-methyl-lanthionine (Thr-Cys) #status experimental
;3-6-42/Cross-link: (25,35,6R)-3-methyl-lanthionine (Thr-Cys) #status experimental
;5-6/Modified site: dehydroalanine (Ser) #status experimental
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ippl. Environ. Microbiol. 58, 3730-3743, 1992

i,Title: Biosynthesis of the lantibiotic nisin: genomic organization and membrane

i,Reference number: A48951; MUID:93128945; PMID:1482192

i,Accession: B48951
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;Reference number: A40621; MUID:93239683; PMID:8478324
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;Residues: 1-57 <KUI>
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Bacteriol. 175, 2578-2588, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                     56;
                                                                                                                                                                                                                                                                                                          MSTKDFNLDLVSVSKKDSGASPRITSTSLCTPGCKTGALMGCNMKTATCHCSIHVSK 57
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larity 98.2%;
Conservative
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Pred. No. 6.9e-27;
0; Mismatches 1
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A; Chan, W.C.; Bycroft, B.W.; Leyland, M.L.; Lian, L.Y.; Roberts,
Biochem. J. 291, 23-27, 1993
Biochem. J. 291, 23-27, 1993
Biochem. J. 291, 23-27, 1993
Biochem. J. 291, 29-27, 1993
Biochem. J. 291, 29-27, 1993
Biochem. J. 291, 1993
B
F;2-24/Domain: propeptide #status predicted <SIG>
F;25-56/Product: subtilin A #status experimental <MATA>
F;25-56/Product: subtilin B #status experimental <MATB>
F;25-56/Product: subtilin B #status experimental <MATB>
F;25-Modified site: succinylated amino end (Trp) (in mature form) #link MATB
F;27-31/Cross-link: sn-(2S,6R)-lanthionine (Ser-Cys) #status experimental
F;29/Modified site: dehydroalanine (Ser) #status experimental
F;29/Modified site: dehydroalanine (Ser) #status experimental
F;37-43/Cross-link: (2S,3S,6R)-3-methyl-lanthionine (Thr-Cys) #status experime;47-50/Cross-link: (2S,3S,6R)-3-methyl-lanthionine (Thr-Cys) #status experime;47-50/Cross-link: (2S,3S,6R)-3-methyl-lanthionine (Thr-Cys) #status experimental
F;49-52/Cross-link: (2S,3S,6R)-3-methyl-lanthionine (Thr-Cys) #status experimental
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A;Experimental source: ATCC 6633
R;Chan, W.C.; Bycroft, B.W.; Leyland, M.L.; Lian, L.Y.; Yang, J.C.; Roberts, FEBS Lett. 300, 56-62, 1992
A;Title: Sequence-specific resonance assignment and conformational analysis o A;Reference number: A44571; MUID:92192284; PMID:1547888
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A;Title: Genes involved in self-protection against the lantibiotic subtilin produced by F
A;Reference number: 140511; MUID:94368094; PMID:8085823
A;Accession: 140514
A;Status: preliminary; translated from GB/EMBL/DDBJ
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R;Klein, C.; Kaletta, C.; Schnell, N.; Entian, K.D.
Appl. Environ. Microbiol. 58, 132-142, 1992
A;Title: Analysis of genes involved in biosynthesis of the lantibiotic subtilin.
A;Reference number: A43935; MUID:92171481; PMID:1539969
A;Accession: D43935
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J. Bacteriol. 174, 1417-1422, 1992
A;Title: The subtilin gene of Bacillus subtilis ATCC 6633 is A;Reference number: A42655; MUID:92138640; PMID:1735728
A;Accession: D42655
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J. Biol. Chem. 263, 9508-9514, 1988
A;Tille: Structure and expression of a gene encoding the A;Reference number: A28112; MUID:88243844; PMID:2837490
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A;Title: Biosynthesis and secretion of a precursor of nisin A;Reference number: S36142; MUID:93380562; PMID:8370453
A;Contents: annotation
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A;Experimental source: ATCC 6633
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A;Residues: 1-56 <CHU>
A;Cross-references: GB:M83944; NID:g143557; PIDN:AAA22772.1;
A;Experimental source: ATCC 6633
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Date: 30-Sep-1989 #sequence revision 12-May-1994 #text change 21-Jul-2000;
Accession: A28112; D42655; D43935; I40514; I39980; S36I42
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R;Allgaier, H.; Jung, G.; Werner, R.G.; Schneider, U.; Zaehner, H. Eur. J. Biochem. 160, 9-22, 1986
A;Title: Epidermin: sequencing of a heterodet tetracyclic 21-peptide A;Reference number: A61287; MUID:87030262; PMID:3769923
A;Accession: A61287
gallidermin precursor - Staphylococcus gallinarum C;Species: Staphylococcus gallinarum C;Species: Staphylococcus gallinarum C;Date: 10-Mar-1994 #sequence revision 12-May-1994 #text_chanc C;Accession: A61072; A44573; A53264 R;Schnell, N.; Entian, K.D.; Goetz, F.; Hoerner, T.; Kellner, FEMS Microbiol. Lett. 58, 263-268, 1989 A;Title: Structural gene isolation and prepeptide sequence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Note: plasmid pEpi32
R;Schnell, N.; Engelke, G.; Augustin, J.; Rosenstein, R.; Ungermann, V.; Goetz, FEur. J. Biochem. 204, 57-68, 1992
A;Title: Analysis of genes involved in the biosynthesis of lantibiotic epidermin. A;Reference number: $23413; MUID:92152237; PMID:1740156
A;Accession: $23415
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A;Title: Prepeptide sequence of epidermin, a ribosomally A;Reference number: S00768; MUID:88216821; PMID:2835685
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Superfamily: subtilin precursor

Reywords: antibiotic; blocked carboxyl end; lanthionine

1-30/Domain: propertide #status predicted <PRO>

1-30/Domain: propertide #status predicted <PRO>

31-52/Product: epidermin #status experimental <MAT>

33-37/Cross-link: sn-(25,6R)-lanthionine (Ser-Cys) #status experimental

34-41/Cross-link: (25,35,RR)-3-methyl-lanthionine (Thr-Cys) #status experimental

34-44/Modified site: (2)-dehydrobutyrine (Thr) #status experimental

34-6-51/Cross-link: sn-(25,6R)-lanthionine (Ser-Cys) #status experimental

34-6-51/Cross-link: (5,Z)-S-(2-aminovinyl)cysteine (Ser-Cys) #status experimental
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;Residues: 31-52 <ALL>
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;Residues: 1-52 <SCH>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 n 31.1%;
Similarity 62.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                    FNLDLVSVSKK---DSGASPRITSTSLCTPGC-KTGA 38
                                                                                                                                                                                                                                                                                                                                             FNLD-VKVNAKESNDSGAEPRIASKFICTPGCAKTGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     59.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 94.5; DB 1; Length 52; Pred. No. 0.00059;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 157; DB 1; Length 56; Pred. No. 5.5e-11; B; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
prepeptide sequence of gallidermin,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0.00059;
                                                                                                                      #text_change 26-Feb-1999
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                                                         R.; Jung, G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PID:g46967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       H.; Kellner,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        54
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amide antibiotic.
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      lanthid
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C;Superfamily: subtilin precursor
C;Keywords: antibiotic; blocked carboxyl end; lanthionine
F;1-30/Domain: propeptide #status predicted <PRO>
F;31-52/Product: gallidermin #status experimental <MAT>
F;33-37/Cross-link: sn-(25,6R)-lanthionine (Ser-Cys) #status experimental
F;38-41/Cross-link: (25,35,6R)-3-methyl-lanthionine (Thr-Cys) #status experimental
F;44/Modified site: dehydrobutyrine (Thr) #status experimental
F;46-51/Cross-link: sn-(25,6R)-lanthionine (Ser-Cys) #status experimental
F;49-52/Cross-link: (5,Z)-S-(2-aminovinyl)cysteine (Ser-Cys) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
S50358
                                      C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision
C;Accession: C82577
C;Accession: C82577
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       문
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A;Title: Gallidermin: a new lanthionine-containing polypeptide antibiotic.
A;Reference number: A44573; MUID:89030695; PMID:3181159
R; anonymous, The Xyı
Nature 406, 151-157,
                                                                                                                   hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Lye, G.; Bowman, S.; Churcher, C. submitted to the EMBL Data Library,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Species: Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: protein A; Residues: 31-52 < KEL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: DNA
A;Residues: 1-995 <LYE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Reference number: S50349
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Gene: MIPS:YIL169c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cross-references: SGD:S0001431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Date: 13-Jan-1995 #sequence_revision 10-Feb-1995
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                                                                                                                                                                                                                                                                                 41 -- GCNMKTATCHCSIHVS 56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23;
    The Xylella fastidiosa
151-157, 2000
                                                                                                                   protein XF2284 [imported] -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S50358
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                                                                                                                                                                                                                                      DNGCNTKTVTSECSKETS 753
                                                                                                                                                                                                                                                                                                                                                                          TKDFNLDLVSVSKKDSGASPRITSTSLCTPGC----KTGALM---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FNLDLVSVSKK---DSGASPRITSTSLCTPGC-KTGA 38
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                                                                                                                                                                                                                                                                                                                                                                                                                                           20.7%;
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Pred. No. 27;
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Pred. No. 0.0013;
                            Consortium
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                                                                     20-Aug-2000 #text_change 20-Aug-2000
                                                                                                                   Xylella fastidiosa
                          of the Organization for Nucleotide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 995
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 21-Jul-2000
C;Accession: T13954
R;Nakayama, M.; Nakajima, D.; Nagase, T.; Nomura, N.; Seki, N.; Ohara, O.
Genomics 51, 27-34, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Experimental source: strain 9a5c
R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A
Briones, M.R.S.; Bleno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H
Briones, B.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
pubmitted to GenBank, June 2000
A; Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm
J.D.; Jungqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigr
Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E
A; Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;
F.G.; Nunes, L.R.; Oliveira, M.G.; de Oliveira, R.C.; Palmieri, D.R.
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak
A; Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveira
M.; Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
B. Beforence number: Ascapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein T23F1.6 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #t C;Accession: T25169
R;Wilkinson, J.
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                                                                                                                                                      MEGF6 protein -
                                                                                                                                                                                                                                                                                                            문
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Map position: A; Introns: 16/3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: EMBL:Z81129; PIDN:CAB03405.1; GSPDB:GN00023; CESP:T23F1.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-330 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Reference number: A; Accession: T25169
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A; Residues: 1-78 <SIM>
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
nes 12; Conserv
                                                                                                                                                                                                                                                                                                            275
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                                                                                                                                                                                                                                                                                                         RTTASQQCAPACSTSCNQSCNQPAQMACQPMQNSQCGCQQNYS 317
                                                                                                                                                                                                                                                                                                                                                             RITSTSLCTPGCKTGALMGCN------MKTATCHCSIHVS 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RPDAVSVLTPGCKQAGATLLTLRVRATLYCSTHI 48
                                                                                                                                                                                                                                                                                                                                                                                                                       19.6%; ilarity 27.9%; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 59.5;
Pred. No. 26;
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Pred. No. 7
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DLVSVSKKDSG-ASPR--

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hypothetical protein F46E10.11 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #tex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: EMBL:X62528; NID:g57670; PIDN:CAA44388.1; PID:g57671 C;Superfamily: ribonuclease inhibitor; leucine-rich alpha-2-glycoprotein F;280-304/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000 C;Accession: S20597  
C;Accession: S20597  
R;Kawanomoto, M.; Motojima, K.; Sasaki, M.; Hattori, H.; Goto, S.
Biochim. Biophys. Acta 1129, 335-338, 1992
B;Title: cDNA cloning and sequence of rat ribonuclease inhibitor, and tissue A;Reference number: S20597; MUID:92162755; PMID:1536887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Title: Identification of high-molecular-weight proteins with multiple EGF-like motifs t A;Reference number: Z14126; MUID:98360089; PMID:9693030 A;Accession: T13954 A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                            A; Reference number: Z21446
A; Accession: T33970
                                                                                                                                                                                                                                                                                                                                                                                                      R;Johnson, D.; Bradshaw, H. submitted to the EMBL Data Library, February 1999 A;Description: The sequence of C. elegans cosmid
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A; Residues: 1-456 < KAW>
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A;Experimental source: strain Sprague-Dawley; brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: mRNA
A; Residues: 1-1574 < NAK>
                                                                                                                                                          A; Introns:
                                                                                                                                                                                                    A; Gene: CESP: F46E10.11
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                                                                                                                                                                                                                                                A: Experimental source:
                                                                                                                                                                                                                                                                          A;Cross-references:
                                                                                                                                                                                                                                                                                             A;Residues: 1-166 <JOH>
                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
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                                                                   Matches
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rons: 55/1
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                                                                                                                                                                                                                                                                                                                                  preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            284 LSLAGNELKDEGA--QLLCESLLEPGCQLESLWVKTCSLTAASCPHFCSV
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                                                                   l Similarity
19; Conser
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Similarity 27.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LDLVSVSKKDSGASPRITSTSLCTPGCKTGAL--MGCNMKTATC--HCSI
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                                                                                                                                                                                                                                              EMBL:AF125955; PIDN:AAD14711.1; GSPDB:GN00023; ce: strain Bristol N2; clone F46E10
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                                                                                      19.2%;
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 Mismatches

                                                                 Score 58.5; D
Pred. No. 19;
4; Mismatches
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Pred. No. 1e+02;
----ITSTSLCTPGCKTGALMGCNMKTATCHCS
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                                                                                                           Length 166;
                                                                   Indels
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                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-565 < STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A;Reference number: A84420; MUID:20083487; PMID:10617197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature 402, 761-768, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Lin, X.; Kaul
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Stifani, S.; Blaumueller, C.M.; Redhead, N.J.; Hill, R.E.; Ar
Nature Genet. 2, 119-127, 1992
A;Tille: Human homologe of a Drosophila enhancer of split gene
A;Reference number: A56695; MUID:93265135; PMID:1303260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        transducin-like enhancer-of-split homolog TLE-3 - human
                                                                                                                                                                                                                                                                                                        Map
                                                                                                                                                                                                                                                                                                                                                                                                                                  Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Reference number: A84420; Accession: F84721
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Residues: 1-772 <STI>
                                                                                                                                                                                                                     Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Accession: F84721
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cross-references: GDB:228049; OMIM:600190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gene: GDB:TLE3; ESG; ESG3
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Date: 21-Jul-1995 #sequence
                                                                                                                                                                                                                                                           Query Match
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                                                                                                                                                                                                                                                                                                     e: At2g31510
position: 2
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                                            LVDPROGTKPELIVCNCTMH 505
                                                                                                                                   SKDFNDFRTKLAGLTSVTKNYFENLVKALENGLADVDSHAACSSKSTSSKSTGCSSKTRE 485
                                                                                                                                                                         STKDFNLDLVSVSKKDSGASPRITSTSLCTPGCKTGALMGCNMKTAT 48
                                                                                      LM----GCNMKTATCHCSIH 54
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y. fat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, n., W.C.; White, O.; Elsen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15pter-15qter
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                                                                                                                                                                                                                                   19.1%;
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homology <WD2>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C.M.; Redhead, N.J.; Hill, R.E.; Artavanis-Tsakonas,
                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                       Score 58;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 58.5;
Pred. No. 71;
                                                                                                                                                                                                                 ed. No. 61;
Mismatches
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phosphoribosylanthranilate isomerase (EC 5.3.1.24) - Lipomyces starkeyi
C;Species: Lipomyces starkeyi
C;Date: 06-Dec-1996 #sequence_revision 25-Apr-1997 #text_change 20-Jun'-
                                                                  S70355
                                                                                      RESULT 15
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C;Reywords: phosphoprotein
F;527-550/Domain: WD repeat homology <WD1>
F;613-646/Domain: WD repeat homology <WD3>
F;695-728/Domain: WD repeat homology <WD4>
F;736-769/Domain: WD repeat homology <WD5>
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A;Title: Molecular cloning and expression of mouse and human A;Reference number: 835678; MUID:93373944; PMID:8365415
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                                                                                                                                                                                                                                                                                    A;Cross-references: EMBL:X73360; NID:g313235; C;Superfamily: unassigned WD repeat proteins;
                                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
A; Residues: 1-771 < MIY>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    F;108-140/Domain: calmodulin repeat homology <EF1>
F;153-185/Domain: calmodulin repeat homology <EF2>
F;264-251/Domain: protein kinase C zinc-binding repeat homology <KZ1>
F;268-317/Domain: protein kinase C zinc-binding repeat homology <KZ2>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    diacylglycerol kinase (EC 2.7.1.107) alpha - rat
C;Species: Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 26-May-2000
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                                            2 STKDFNLDLVSVSKKDSGASPRITSTSLCTPGCKTGALMGCNMKTAT
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Brain Res. 16, 75-87, 1992
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#sequence\_revision 25-Apr-1997 #text\_change 20-Jun-2000

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C;Accession: S70355
CLRT. Genet. 30, 83-88, 1996
A;Title: Electrophoretic karyotype of the amylolytic yeast Lipomyces starkeyi and clonin A;Accession: S70355
A;Cors. Genet. 30, 83-88, 1996
A;Accession: S70355
A;Molecule type: DNA
A;Reference number: S70355; MUID:96269934; PMID:8662214
A;Accession: S70355
A;Molecule type: DNA
A;Residumes 1-232 **CBIG*
A;Cross-references: EMBL:Z68292; NID:g1134847; PIDN:CAA92584.1; PID:g1161576
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Result
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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304
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Gapop 10.0 , Gapext 0.5
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                                          SwissProt_41:*
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P10946 bacillus su
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P21838 staphylococ
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P40442 saccharomyc
P29315 rattus norv
P5947 helix pomat
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Q081441 mus musculu
Q07141 rattus norv
Q62441 mus musculu
Q27591 drosophila
Q03376 chironomus
Q9976 bomo sapien
Q64727 homo sapien
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## ALIGNMENTS

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EMBL; J04057; AAA88606.1; ...
EMBL; M65089; AAA73038.1; ...
EMBL; M24527; AAA26948.1; ...
EMBL; X68307; CAA48380.1; ...
EMBL; M27277; AAA25188.1; ...
EMBL; D00696; BAA00602.1; ...
EMBL; L16226; AAA25189.1; ...
EMBL; M79445; AAA25189.1; ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tabeling of bacteriocins: NMR resonance assignments of leucocin A from Leuconostoc gelidum and nisin A from Lactococcus lactis."; Biochemistry 32:310-318(1993).

-I- FUNCTION: LANTHIONINE-CONTAINING PEPTIDE ANTIBIOTIC (LANTIBIOTIC) ACTIVE ON GRAM-POSITIVE BACTERIA. THE BACTERICIDAL ACTIVITY OF LANTIBIOTICS IS BASED ON DEPOLARIZATION OF ENERGIZED BACTERIAL CYTOPLASMIC MEMBRANES, INITIATED BY THE FORMATION OF AQUEOUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=93202265; PubMed=8454055; MEDLINE=93202265; PubMed=8454055;
                                                PIR;
                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 24-57.
MEDLINE=72072901; PubMed=5131162;
Gross E., Morell J.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                aqueous environments." FEBS Lett. 319:189-194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           van den Hooven H.W., Fogolari F., Ro
Hilbers C.W., van de Ven F.J.;
"NMR and Circular dichroism studies
                                                                                                                                                                                                                                                                                                                                       entities requires
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"NMR studies of lantibiotics. The structure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRUCTURE
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MISCELLANEOUS: USED AS A FOOD PRESERVATIVE.

MISCELLANEOUS: USED AS A FOOD PRESERVATIVE OF CHROMOSOMAL AND PLASMID DNA. THE SEQUENCES REPORTED ARE ABSOLUTELY IDENTICAL.

SIMILARITY: STRUCTURAL SIMILARITY TO OTHER TYPE A LANTIBIOTICS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TRANSMEMBRANE PORES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lett. 319:189-194(1993).
                                                A31915;
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n. Chem. Soc. 93:4634-4635(1971).
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ein cross-linking, p
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                                                                                                                                                                                                                                                                                                          s requires a license agreement (S an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Biochem.
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G.L., Henkel T.,
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4.C., Morley S.D.,
Lan dom.
Nisīn.
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SEQÜENCE
                                                                                                                                                                                                                                          MEDLINE=95352820; PubMed=7626780; Timmonen T., Ye S., Ra R., Olao M., Paulin L., Saris P.E.J. Timmonen T., Ye S., Ra R., Olao M., Paulin L., Saris P.E.J. Timmonen T., Ye S., Ra R., Olao M., Paulin L., Saris P.E.J. Timmonen T., Ye S., Tanker P.E.J. Timmonen T., Paulin L., Saris P.E.J. Timmonen T., Paulin L., Paulin L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN=NIZO 22186;
MEDLINE=92037612; PubMed=1935953;
Milders J.W.M., Boerrigter I.J., 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LACLA
                                                                                                                                                                                                                         transposon.";
                                                                                                                                                                                                                                                                                                                                                                                                               Rraya T., Ishibashi N., "Genetic evidence that
                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=JCM 7638;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lactococcus lactis (subsp. Bacteria; Firmicutes; Lacto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-APR-1993
15-SEP-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Vos W.M.;
                                                                                                                  Seq. 5:203-218(1995).

Seq. 5:203-218(1995).

FUNCTION: LANTHIONINE-CONTAINING PEPTIDE ANTIBIOTIC (LANTIBIOTIC)

ACTIVE ON GRAM-POSITIVE BACTERIA. THE BACTERICIDAL ACTIVITY OF

LANTIBIOTICS BASED ON DEPOLARIZATION OF ENERGIZED BACTERIAL

CYTOPLASMIC MEMBRANES, INITIATED BY THE FORMATION OF AQUEOUS
               and cleavage of the moc
SIMILARITY: STRUCTURAL
                                  PTM: Maturation of lantibiotics involve thr, and Ser into dehydrated AA and tho bonds with cysteine. This is followed and cleavage of the modified precursor
                                                                                                                TRANSMEMBRANE PORES.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TaxID=1360;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     56;
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nisin Z pr
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Lactobacillales; Streptococcaceae; Lactococcus
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Last annotation updat
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DHB (2,3-DIDEHYDROBUTYRINE).
DHA (2,3-DIDEHYDROALANINE).
DHA (2,3-DIDEHYDROALANINE).
315E4428AC70BFEA CRC64;
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Pred. No. 8.2e-31;
); Mismatches 1
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Beta-methyllanthionine
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brane translocation
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(Thr-Cys).
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15-SEP-2003
Lantibiotic
                                                                                                                                                                                                                                                                                                                                             LT 3
_BACSU
_LANS_E
                                                                               STRAIN=ATCC 6633 / LITTLE 92138640; PubMed=1735728;
Chung Y.J., Steen M.T., Hansen J.N.;
"The subtilin gene of Hacillus subtilis ATCC 6633 is encoded "The subtilin gene of Hacillus subtilis ATCC 6633 is encoded the subtilin gene of Hacillus subtilis ATCC 6633 is encoded the subtilin gene of Hacillus subtilis ATCC 6633 is encoded the subtiling a homolog of the hemolysin B transport
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                                                                                                                                                                                                                                                         Bacillus subtilis.
Bacteria; Firmicutes;
"Analysis of subtilin.";
                  STRAIN=ATCC 6633 / LH45;
MEDLINE=92171481; PubMed=1539969;
Klein C., Kaletta C., Schnell N.,
                                                                                                                                      SEQUENCE FROM N.A. STRAIN=ATCC 6633 /
                                                                                                                                                                                subtilin,
                                                                                                                                                                                                     Banerjee
                                                                                                                                                                                                              MEDLINE=88243844; PubMed=2837490;
                                                                                                                                                                                                                                                                                 SPAS
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                                                    EQUENCE
                                                                         Bacteriol.
                                                                                                                                                                       Biol.
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                                                                                                                                                                                   e S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
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                                                    FROM
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(Rel. 11,
(Rel. 42,
subtilin
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          genes
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                                                                        174:1417-1422(1992)
                                                                                                                                                                     expression of a gene encoding all protein antibiotic."; 263:9508-9514(1988).
                                                                                                                                                                                                                                                                                                                                              STANDARD;
           involved
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96.5%;
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                                                                                                                                                                                                                                                         Bacillales;
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          ll N., Entian K.-D.;
in biosynthesis of the
                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 291; DB Pred. No. 6.2e 1; Mismatches
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Beta-methyllanthionine (Thr-Cys).
DHB (2,3-DIDEHYDROBUTYRIB).
DHA (2,3-DIDEHYDROALANINE).
DHA (2,3-DIDEHYDROALANINE).
N->H (IN STRAIN JCM7638).
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Beta-methyllanthionine
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EMBL; J03767; AAA22840.1; -.
EMBL; M86869; AAA22840.1; -.
EMBL; M83944; AAA22772.1; -.
EMBL; M939263; AAA22778.1; -.
EMBL; U09819; AAB91589.1; -.
PIR; A28112; NIBSSA.
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                                                                                                                                                        Pfam; PF02052; Gallidermin; PRINTS; PR00324; NISIN.
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Gross E., Kiltz H.H.,
"Subtilin, VI: the st:
                                                                                                                                         PRINTS; PRO(
Antibiotic;
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MEDLINE=93167833; Pub
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Gross E., Kiltz H.H., Nebelin E.;
"Subtilin, VI: the structure of subtilin.";
Hoppe-Seyler's Z. Physiol. Chem. 354:810-81
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Thr, and Ser into dehydrated AA and the formation of thi bonds with cysteine. This is followed by membrane transl and cleavage of the modified precursor.
MISCELLANEOUS: SUBTILIN ACTIVITY IS OBSERVED DURING STATEMASE, BUT NOT DURING EXPONENTIAL GROWTH.
SIMILARITY: STRUCTURAL SIMILARITY TO OTHER LANTIBIOTICS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PTM: Maturation of lantibiotics involves the enzymic conversion Thr, and Ser into dehydrated AA and the formation of thioether bonds with cysteine. This is followed by membrane translocation
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FUNCTION: LANTHIONINE-CONTAINING PEPTIDE ANTIBIOTIC (LANTIBIOTIC)
ACTIVE ON GRAM-POSITIVE BACTERIA. THE BACTERICIDAL ACTIVITY OF
LANTIBIOTICS IS BASED ON DEPOLARIZATION OF ENERGIZED BACTERIAL
CYTOPLASMIC MEMBRANES, INITIATED BY THE FORMATION OF AQUEOUS
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Bycroft B.W., Leylands M.L.,
                                                                                                                                           Bacteriocin;
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      Nisin.
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                                                                                                                                         Lantibiotic; D-amino acid; Thioether bond
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              Lanthionine (Ser-Cys).

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Beta-methyllanthionine (Thr-
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Beta-methyllanthionine (Thr-
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PO8136; Q54093;
01-AUG-1988 (Rel. 08, Created)
01-AUG-1988 (Rel. 08, Last seg
15-SEP-2003 (Rel. 42, Last ann
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                                                        EMBL; X07840; CAA30689.1; -.
EMBL; X07840; CAA30690.1; -.
EMBL; X62386; CAA4252.1; -.
EMBL; X62386; CAA01070.1; -.
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the European Bioinformatics Institute. There are no restrictions on
use by non-profit institutions as long as its content is in no
modified and this statement is not removed. Usage by and for commer
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MEDLINE=92155237; PubMed=1740156;
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Bacteria; F:
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"Analysis of genes involved in the biosynthesis
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                 nterPro;
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SIMILARITY: STRUCTURAL SIMILARITY TO OTHER TYPE A LANTIBIOTICS.
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IPR006078; Gallidermin.
IPR006079; Lan_dom.
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                                                                                                                                          license agreement
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Pred. No.
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                    PIR; A61072; EPSGD.
InterPro; IPR006078; Gallidermin.
InterPro; IPR006079; Lan_dom.
InterPro; Gallidermin; 1.
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SEQUENCE
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Staphylococcus gallinarum.
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15-SEP-2003
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            PRINTS; PR00323;
                                                                                                                                                                                                                                                                                                                                   Kellner
                                                                                                                                                                                                                                                                                                                                                             STRAIN=TU
                                                                                                                                                                                                                                                                                                                                                                                           Schnell N., Entian K.-D., Goetz F., Hoerner T., Kellner R., Jung G "Structural gene isolation and prepeptide sequence of gallidermin, new lanthionine containing antibotic.";
FEMS Microbiol. Lett. 49:263-267(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE=89306540; PubMed=2765032;
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                                                                                                                                                                                                                      'The solution structure of the lantibiotic gallidermin.";
                                                                                                                                                                                                                                    Werner R.
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                                                                                                                                                                                                                                                                                                                                                                       EQUENCE
                                                                    Thr, and Ser into dehydrated AA and the formation of thioether bonds with cysteine. The C-terminal lanthionine undergoes decarboxylation. This is followed by membrane translocation and cleavage of the modified precursor.

SIMILARITY: STRUCTURAL SIMILARITY TO OTHER TYPE A LANTIBIOTICS.
                                                                                                                                                       FUNCTION: LANTHONINE-CONTAINING PEPTIDE ANTHBIOTIC (LANTHBIOTIC) ACTIVE ON GRAM-POSITIVE BACTERIA. THE BACTERICIDAL ACTIVITY OF LANTIBIOTICS IS BASED ON DEPOLARIZATION OF ENERGIZED BACTERIAL CYTOPLASMIC MEMBRANES, INITIATED BY THE FORMATION OF AQUEOUS
                                                                                                                                  TRANSMEMBRANE PORES.

PTM: Maturation of lantibiotics involves the enzymic
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gallidermin precursor.
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            GALLIDERMIN.
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Lantibiotic;
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Pred. No. 2.
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Beta-methyllanthionine
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8B1AD2875BF16D6D CRC64;
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S-(2-aminovinyl)-D-cysteine
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D-amino acid;
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.2e-05;
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MEDLINE=21192684; PubMed=11296296;

Ferretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K., Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P., Qian Y., Jia H.G., Najar F.Z., Ren Q., Zhu H., Song L., White J., Yuan X., Clifton S.W., Roe B.A., McLaughlin R.;

Yuan X., Clifton S.W., Roe B.A., McLaughlin R.;

"Complete genome sequence of an M1 strain of Streptococcus pyogenes.";
                                                                                                                                                                                                                                                                                                                                                                                                      Karaya K., Taketo A.; "Gene cluster of lantibiotics producing by Streptococcus pyogenes."; Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
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                                                                                                         CHAIN
                                                                                                                                            EMBL; AB030831; BAB08162.1; -. EMBL; AE006552; AAK33966.1; -.
                                                                                                                                                                  entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                     the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for commodified
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16-OCT-2001 (Rel. 40, Last
Lantibiotic srtA precursor.
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Q9FDV1;
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                                                                                                                       PROPEP
                                                                                                                                 Antibiotic;
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KDFDLDL-KTNKKDT-ATPYVGSRYLCTPG
                     KDFNLDLVSVSKKDSGASPRITSTSLCTPG 33
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ilarity 62.2%;
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                                            Score 72; DB
Pred. No. 0.01
5; Mismatches
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Pred. No. 5.2e
3; Mismatches
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S-(2-aminoviny1)-D-cysteine (Ser-Cys).
DHB (2,3-DIDEHYDROBUTYRINE).
                                                                                            LANTIBIOTIC SRTA.
3775CC54B8A2B00F
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Best Local :
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16-OCT-2001 (Rel. 40, C
16-OCT-2001 (Rel. 40, L
15-SEP-2003 (Rel. 42, L
Band 4.1-like protein 5
EPB41L5 OR KIAA1548.
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CARBOHYD
CARBOHYD
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SGD; S0001431; YII169C.
THERPTO; IPRO04089; Chmtaxis_TRANSDUC_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     use by non-profit institute. There are no rest modified and this statement is not removed. Usage by an entities requires a license agreement (See http://www.i---or send an email to license.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Churcher C.M., Bowman S., Badcock K., Bankier A., Brown D., Chillingworth T., Connor R., Devlin K., Gentles S., Hamlin N., Harris D.E., Horsnell T., Hunt S., Jagels K., Jones M., Lye G., Moule S., Odell C., Pearson D., Rajandream M.A., Rice P., Rowley Skelton J., Smith V., Walsh S., whitehead S., Barrell B.G.; "The nucleotide sequence of Saccharomyces cerevisiae chromosome Nature 387:84-87(1997).
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01-FEB-1995 (Rel. 31, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Hypothetical 99.7 kDa protein in SDL1 5'region
YIL169C OR YI9402.07C.
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Eukaryota; Metazoa;
Mammalia; Eutheria;
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                           Homo sapiens (Human)
                                                                                                                         E4L5 HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
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Chordata;
Primates;
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                                                                                                                                                                                                                                                                                                                                                               99735 MW;
                                                                   Last annotation
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HYPOTHSTICAL PROTEIN YIL169C.

METHYL-ACCEPTING TRANSDUCER.

N-LINKED (GLCNAC. . .) (POTENT)

N-LINKED (GLCNAC. . .) (POTENT)
                                                                                  sequence
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Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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the European Bioinformatics Institutions as long a
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modified and this statement is not removed.
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code for large proteins in vitro.";
DNA Res. 7:273-281(2000) 1 FERM dom
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PROSITE; PS00661; FERM_2; 1.
PROSITE; PS50057; FERM_3; 1.
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                                                                                                   Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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01-DEC-1992 (Rel.
28-FEB-2003 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000299; Band_4.1.
Pfam; PF00373; Band_41; 1.
PRINTS; PR00935; BAND41.
SMART; SM00295; B41; 1.
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N1shikawa T., Nagai K., Sugano S., Aotsuka S., Yoshikawa
Matsunawa H., Ishii S., Kawai Y., Saito K., Yamamoto J.,
Nakamura Y., Nagahari K., Masuho Y., Sasaki N.;
"NEDO human cDNA sequencing project.";
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
                                                          SEQUENCE FROM N.A., AND PARTIAL SEQUENCE
                                                                                     NCBI_TaxID=10116;
                                                                                                                                                                                                                          P29315;
                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-20450683; PubMed-10997877;
Nagase T., Kikuno R., Nakayama M., Hirosawa M., Ohara O.;
"Prediction of the coding sequences of unidentified human genes.
XVIII. The complete sequences of 100 new cDNA clones from brain which
                                          TISSUE=Lung;
                                                                                                                                   Rattus norvegicus (Rat)
                                                                                                                                                                 Ribonuclease
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
               Kawanomoto M., Motojima K.,
                              MEDLINE=92162755; PubMed=1536887;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
[1]
                                                                                                                                                                                                                                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: Contains 1 FERM domain.
                                                                                                                                                                                                                                                                                                                 631
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                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                         STKDFNLDLVSVSKK--DSGASPRITSTSLCTP-----GCKTGALMGCNM
                                                                                                                                                                                                                                                                                                              ATDELDALLASLTENLIDHTVAPQVSSTSMITPRWIVPSGAMSNGLAGCEM 681
                                                                                                                                                                                                                                                                                                                                                                                                                                 732 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           43
669
                                                                                                                                                                               (Rel.
                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                        STANDARD;
tojima K., Sasaki M., Hattori H., Goto S sequence of rat ribonuclease inhibitor,
                                                                                                                                                                         24, Created)
24, Last sequence up
41, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           327
732
                                                                                                                                                                                                                                                                                                                                                                                                                                 81758 MW;
                                                                                                                                                                                                                                                                                                                                                                                      20.1%;
                                                                                                                                                                                                                                                                                                                                                                        12;
                                                                                                                                                                                                                                                                                                                                                                     Score 61; DB 1
Pred. No. 5.9;
12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                              TSSGPILAEEAVLKQKCLLTTEL -> VFTDH (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SGAMSNGLAGCEMLLTGKEGHGNKDGISLISPPAPFLVDAV
                                                                                                                                                                                                                                      PRT;
                                                                                                    Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                 76D5BD8CE099E761 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Aotsuka S., Yoshikawa Y.,
Saito K., Yamamoto J., Wakamatsu A.,
., Sasaki N.;
                                                                                                                                                                                             update)
                                                                                                                                                                                                                                        456
                                                                                                                                                                              update)
                                                                                                                                                                                                                                                                                                                                                                                                    DB 1;
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                                                                                                                                                                                                                                                                                                                                                                                                  Length 732;
                                                                                                                                                                                                                                                                                                                                                                        Indels
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                                                                                                      Murinae; Rattus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              LWSHFGRRSCPEAE
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and tissue
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RESULT 10
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Best Local
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PIR, S20597; S20597.
HSSP; P10775; ZBHH.
InterPro; IPR001611; LRR.
InterPro; IPR007091; LRR. RNinh.
InterPro; IPR003590; LRR. RNinh.
Pf6am; PF00560; LRR; 4.
SMART; SM00368; LRR, RI; 1.
                                                                                                  01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update
Copper-metallothonein (Cu-MT).
Helix pomattia (Roman snail) (Edible snail).
Eukaryota; Metazoa; Mollusca; Gastropoda; Pu
Sigmurethra; Helicoidea; Helicidae; Helix.
                                                                                                                                                                                                                                                                                                                                                   REPEAT
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SEQUENCE
                                                                                                                                                                                     MTCU_HELPO
P55947;
         MEDLINE=97373947; PubMed=9230430;
Dallinger R., Berger B., Hunziker P.E., Kaegi J.H.R.;
"Metallothionein in snail Cd and Cu metabolism.";
Nature 388:237-238(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                          REPEAT
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REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for conmodified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This
                                                         SEQUENCE.
TISSUE=Mantle;
                                                                                                                                                                                                              HELPO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entities requires a
                                                                                                                                                                                                                                                                                                                                                                                                                                                           REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHAM. BIODAYS. ACTS 1129.335-338(1992).
FUNCTION: INHIBITOR OF PANCREATIC RNASE AND ANGIOGENIN. MAY ALSO FUNCTION IN THE MODULATION OF CELLULAR ACTIVITIES.
SUBGUNIT: FORMS A TIGHT ONE-TO-ONE COMPLEX WITH THE RNASE.
SUBCELLULAR LOCATION: Cycoplasmic.
SUBCELLULAR LOCATION: Cycoplasmic.
TISSUE SPECIFICITY: BRAIN, HBART, LUNG, LIVER, SPLEEN, TESTES AND LOWEST IN THE HEART.
KIDNEY; HIGHEST IN THE LUNG AND LOWEST IN THE HEART.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: Contains 15 leucine-rich (LRR) repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SWISS-PROT entry is copyright. It is produced through a deen the Swiss Institute of Bioinformatics and the EMBL
                                                                                            TaxID=6536;
                                                                                                                                                                                                                                                         284 LSLAGNELKDEGA--QLLCESLLEPGCQLESLWVKTCSLTAASCPHFCSV
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                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Leucine-rich
                                                                                                                                                                                                                                                                               LDLVSVSKKDSGASPRITSTSLCTPGCKTGAL--MGCNMKTATC--HCSI
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                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                  STANDARD;
METALLOTHIONEINS ARE INVOLVED IN THE CELLULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tatement is not removed. Usage by and for commercial license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                      49905 MW;
                                                                                                                                                                                                                                                                                                                 19.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         repeat.
                                                                                                                                                                                                                                                                                                       8
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                                                                                                                                                                                                                                                                                                                                                    LRR A8.
8518E5B1F09E5998 CRC64;
                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                       Mismatches
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                                                                                                                                                                                                  64
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                                                                                                                  Pulmonata; Stylommatophora;
                                                                                                                                                                                                                                                                                                                             1; Length 456;
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                                                                                                                                                                                                                                                                                                    indels
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Best Local S
Matches 12
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                                                                      MEDLINE=20450683; PubMed=10997877;
Nagase T., Kikuno R., Nakayama M., Hirosawa M., Ohara O.;
"Prediction of the coding sequences of unidentified human
XVIII. The complete sequences of 100 new cDNA clones from
code for large proteins in vitro.";
DNA Res. 7:273-281(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HUMAN
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METAL
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Stifani S., Blaumueller C.M., Redhead N.J., Hill R.E., Artavanis-Tsakonas S.; Redhead N.J., Hill R.E., "Human homologs of a Drosophila enhancer of split gene product define a novel family of nuclear proteins.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Fetal brain;
MEDLINE=93265135; P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                METAL
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                                                                                                                                                                                                                                                                                                                                               TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TLE3 OR KIAA1547.
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: BELONGS TO THE METALLOTHIONEIN SUPERFAMILY; FAMILY 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       METALLOTHIONEINS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ily of nuclear proteins.";
2:119-127(1992).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PubMed=1303260;
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(ISOFORMS 3 AND 4)
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Pred. No. 0.87;
3; Mismatches 6;
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96CC1998B7E12297 CRC64;
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RX MEDLINE=22388257; PhbMed=12477932;

RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RX Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopking R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Hopking R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Hopking R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Hopking R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Biatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Babas S.J., Koguellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Robas S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Rahas S.A., McEwan J.J., McKernan K.J., Malek J.A., Gibbs R.A.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Habey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

RA Habey J., Helton E., Touchman J.W., Green E.D., Dickson M.C.,

RA Balterfield Y.S.N., Krzywinski M.I., Schmutz J., Myers R.M.,

"Generation and initial analysis of more than 15,000 full-length

Thuman and mouse cDNA sequences.",

"Generation and initial analysis of more than 15,000 full-length

Thuman and mouse cDNA sequences.",

"The College A.C., U.S.A., 99:16899-16903 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                    IsoId=Q04726-4; Sequence=VSP_007023, VSP_007024, VSP_006790;
-!- TISSUE SPECIFICITY: Placenta and lung.
-!- SIMILARITY: Contains 7 WD repeats.
-!- SIMILARITY: BELONGS TO THE GROUCHO/TLE FAMILY OF WD-REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SUBUNIT: Homooligomer and heterooligomer with other family
members. Binds LEF1, TCF7, TCF7L1 and TCF7L2 (By similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila groucho, interact with hepatic nuclear factor 3beta.";
J. Biol. Chem. 275:18418-18423 (2000).

1. FUNCTION: Transcriptional corepressor that binds to a number of transcription factors. Inhibits the transcriptional activation mediated by CTNNB1 and TCF family members in Wnt signaling. The effects of full-length TLE family members may be modulated by association with dominant-negative AES (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Transducin-like enhancer of split proteins, the human homologs 
Drosophila groucho, interact with hepatic nuclear factor 3beta."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IsoId=Q04726-3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IsoId=Q04726-2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IsoId=Q04726-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    isoforms;
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Waltner-Law M., Yamada K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: Nuclear.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence=VSP_006789, VSP_006790,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence=VSP_006788;
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EMBL; BC015729; -; NOT\_ANNO; EMBL; BC041831; AAH41831.1; EMBL; M99438; AAA61194.1; EMBL; AB046767; BAB13373. use by non-profit institutions as long a modified and this statement is not removed. entities requires a license agreement (See lor send an email to license@isb-sib.ch). This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Ew the European Bioinformatics Institute. There are no restruces by non-profit institutions as long as its content PIR; D56695; D56695. Genew; HGNC:11839; T GO:0005634; GO:0007397; ,600190; C:nucleus; TAS. P:histogenesis ANNOTATED\_CDS. and organogenesis; TAS (See http://www.isb-sib. Usage by and for commercia 8

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P51576;
P515776;
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Pfam; PF003920; WD40; 6.

ProDom; PD000018; WD40; 1.

SMART; SM0320; WD40; 7.

SMART; SM0320; WD_REPEATS_1; 2.

PROSITE; P$500878; WD_REPEATS_2; 2.

PROSITE; P$50082; WD_REPEATS_REGION; 2.

PROSITE; P$50294; WD_REPEATS_REGION; 2.

PROSITE; P$50294; WD_REPEATS_REGION; 2.

WD_repeat; Phosphorylation; Wnt signaling pathway;

WD_repeat; Phosphorylation; Wnt signaling pathway;
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                                                                                                                                                                                                                                                                                    267
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  Chordata; Craniata; Vertebrata; Euteleostomi;
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38.3%;
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NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
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WD 2.
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6; Mismatches
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erol kinase)
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Matches 16
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ProDom; PD005043; DAGKC; 1.
ProDom; PD005012; EF-hand; 1.
SMART; SM00109; C1; 2.
SMART; SM00045; DAGKA; 1.
SMART; SM00046; DAGKC; 1.
SMART; SM00054; EFh; 2.
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SEQUENCE
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CA_BIND
CA_BIND
DOMAIN
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Transferase; Kinase; Calcium-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00130; DAG PE-bind; 2. Pfam; PF00609; DAGKa; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a cheveen the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Goto K., Watanabe M., Kondo H., Yuasa H., Sakane F., Kanoh H.;
"Gene cloning, sequence, expression and in situ localization of 80 kDa diacylglycerol kinase specific to oligodendrocyte of rat brain.";
Brain Res. Mol. Brain Res. 16.75-87(1992).
-!- FUNCTION: UPON CELL STIMULATION CONVERTS THE SECOND MESSENGER DIACYLGLYCEROL INTO PHOSPHATIDATE, INITIATING THE RESYNTHESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00036; efhand;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR002219; DAG PB-bind.
InterPro; IPR002756; DAGKG.
InterPro; IPR001206; DAGKG.
InterPro; IPR002048; EF-hand.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; S49760; AAB24434.1; -. PIR; A56879; A56879.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entities requires a license agreement (S or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PHOSPHORYLATED BY PROTEIN KINASE C (BY SIMILARITY). SUBUNIT: Monomer (By similarity).
TISSUE SPECIFICITY: LYMPHOCYTES AND OLIGODENDROGLIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   diacylglycerol 3-phosphate.
ENZYME REGULATION: STIMULATED BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACTIVITY: ATP + 1,2-diacylglycerol = ADP + 1,2-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: Contains 2 EF-hand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: Contains 2 zinc-dependent phorbol-ester and
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EF-HAND 2 (PROBABLE).
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PHORBOL-ESTER AND DAG BI
CATALYTIC-B (POTENTIAL).
CATALYTIC-B (POTENTIAL).
                                                  9
                                                                       Score 57.5;
Pred. No. 16;
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Q9JIT3;
15-SEP-2003 (Rel. 42, Created)
15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
15-SEP-2003 (Rel. 42, Last annotation update)
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J. Neurochem. 74:1838-1847(2000).

-!- FUNCTION: Transcriptional corepressor that binds to a
-!- FUNCTION: Transcriptional ac
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DOMAIN
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Pfam; PF00400; WD40; 6.

Prodom; PD0000018; WD40; 1.

SMART; SM00320; WD40; 7.

PROSITE; PS00678; WD REPEATS 1; 2.

PROSITE; PS50082; WD REPEATS 2; 2.

PROSITE; PS50294; WD REPEATS REGION; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entities requires a license agreement (See http://www.isb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                               WD repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR005617; TLE N. InterPro; IPR001680; WD40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AF186092; AAF75590.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Feldman J.D.,
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                                                                                                                                                                                                                                                            Transcription
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: Nuclear.

SUBCELLULAR LOCATION: Nuclear.

TISSUE SPECIFICITY: Highly expressed in adrenal gland, intestine, kidney, lung, ovary and thyroid. Detected at levels in pitultary, hippocampus, cortex, cerebellum ar INDUCTION: By kainic acid in the dentate gyrus.

SIMILARITY: Contains 7 WD repeats.

SIMILARITY: BELONGS TO THE GROUCHO/TLE FAMILY OF WD-RE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - Buropean Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mediated by CTNNB1 and TCF family members in Wnt signaling. The effects of full-length TLE family members may be modulated by association with dominant-negative AES (By similarity). SUBUNIT: Homooligomer and heterooligomer with other family members. Binds LEF1, TCF7, TCF7L1, TCF7L2 and FOXA2 (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           a newly identified transducin-like
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RA OKazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S., RA Vagi K., Tomaru Y., Hasegawa Y., Nogami A., Schombach C., Gojobori T., Ra Haldarelli R., Hill D.P., Bult C., Hume D.A., Ouackenbush J., Ra Baldarelli R., Hill D.P., Bult C., Hume D.A., Ouackenbush J., Ra Baldarelli R., Hill D.P., Bult C., Hume D.A., Ouackenbush J., Ra Baldarelli R., Lyragani T.A., Matsuda H.A., Batalov S., Beisel K.W., Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S., Ra Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S., Ra Balla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S., Ra Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D., Ra Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L., Kawasawa Y., Kedzierski R.M., King B.L., Kawasawa Y., Kedzierski R.M., King B.L., Ra Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H., Ra Wagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G., Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S., Sandelin A., Schneider C., Semple C.A., Secou M., Shimada K., Valanda K., Schoneider C., Semple C.A., Secou M., Shimada K., Valanda R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M., Varardo R., Waynehaw-Boris A., Yanagisawa M., Yang I., Yang L., Ra Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N., Yang L., Shaka K., Sasaki D., Shibata K., Shinagawa A., Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J., Ra Miraki T., Waki K., Sasaki D., Shibata K., Shinagawa A., Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J., Rature 420:563-573 (2002).
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STRAIN=CD-1;
MEDLINE=93373944; PubMed=8365415;
MEDLINE=93373944; PubMed=8365415;
Miyasaka H., Choudhury B.K., Hou E.W., Li S.S.-L.;
Miyasaka H., Choudhury B.K., Li S.S.-L.;
Miyasaka H., Choudhury
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Mammalia; Eutheria;
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STRAIN=C57BL/6J; TISSUE=Testis;
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Last annotation updat
cer protein 3 (ESG) (G
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Pred. No. 17;
6; Mismatches
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(POTENTIAL).
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RC TISSUE-Breast tumor;

RX MEDLINE-22388557; pubMed=12477932;

RX MEDLINE-22388557; pubMed=12477932;

RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RX Alausner R.D., Collins F.S., Wagner L., Schaefer C.F., Bhat N.K.,

RX Alausner R.D., Collins F.S., Wagner L., Schaefer C.F., Bhat N.K.,

RX Alteschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RX Alteschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RX Alteschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RX Alteschulo L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RX Alteschuko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RX Alteschuko L., Marusina K.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RX Alteschuko L., Marusina K.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RX Alteschuko L., Marusina K.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RX Alteschuko L., Marusina K.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RX Alteschuko L., Marusina N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RX Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

RX Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RX Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RX Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RX Alteschuko L., Grimwood J., Schmutz J., Myers R.M.,

RX Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

RX Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

"Generation and mouse cDNA semences ":

**Thuman and mouse cDNA semences ":
                                                                                                                                                                                          EMBL; X73360; CAA51770.1; -. EMBL; AK031322; BAC27347.1; -. EMBL; AK031322; BAC27347.1; -.
                                                                                                                                                                                                                                                                       the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic Acids Res. 29:1410-1419 (2001).

-!- FUNCTION: Transcriptional corepressor that binds to a number of transcription factors. Inhibite transcriptional activation mediated by CINNB1 and TCF family members in Whit signaling. The effects of full-length TLE family members may be modulated by association with dominant-negative AES (By similarity). May play
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      +
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                                                               InterPro; IPR005617; TLE N.
InterPro; IPR001680; WD40.
Pfam; PF03920; TLE N; 1.
Pfam; PF00400; WD40; 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Brantjes H., Roose J., van De Wetering "All Tcf HMG box transcription factors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INTERACTIONS WITH LEF1; TCF7; TCF7L1 AND MEDLINE=21169341; PubMed=11266540;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        human and mouse cDNA sequences."
                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 323-771 FROM N.A. (ISOFORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Note=No experimental confirmation available;
TISSUE SPECIFICITY: Expressed only in testis.
SIMILARITY: Contains 7 WD repeats.
SIMILARITY: BELONGS TO THE GROUCHO/TLE FAMILY OF WD-REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION: Nuclear.
ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Na
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             an important role during spermatogenesis.
SUBUNIT: Homooligomer and heterooligomer with other family
members. Binds FOXA2 (By similarity). Binds LEF1, TCF7, TC
                                                                                                                                                     S35681; S35681.
MGI:104634; Tle3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IsoId=Q08122-1; Sequence=Displayed;
                        PD000018;
; PS00678;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          [soId=Q08122-2; Sequence=VSP_007025;
                                                                                                                                                                                                                                                                                                                                                                                         the Swiss Institute
WD40; 1.
WD_REPEATS_1;
WD_REPEATS_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      confirmation available;
                                                                                                                                                                                                                                                                                                                                                                                       of Bioinformatics
                                                                                                                                                                                                                                                                                                                                                                                                           It is produced through
                                                                                                                                                                                                                                                                                                      (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           M., Clevers H. interact with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2)
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                                                                                                                                                                                                                                                                                                                     Usage
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RESULT
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Best Local :
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                                                                                                                                                                                                                                                                                                                                      ENTK MOUSE
P97435;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CONFLICT
SEQUENCE
                                                                                                     small intestine during development.";
Am. J. Physicl. 274:G342-G349(1998).
-i- FUNCTION: RESPONSIBLE FOR INITIATING ACTIVATION OF PANCREATIC
-i- FROTEOLYTIC PROENZYMES (TRYPSIN, CHYMOTRYPSIN AND CARBOXYPEPTIDASE
A). IT CATALYZES THE CONVERSION OF TRYPSINGOEN TO TRYPSIN WHICH IN
TURN ACTIVATES OTHER PROENZYMES INCLUDING CHYMOTRYPSINGEN,
PROCARBOXYPEPTIDASES, AND PROELASTASES (BY SIMILARITY).
-i- CATALYTIC ACTIVITY: Selective cleavage of 6-Lys-|-Ile-7 bond in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOD_RES
                                                                                                                                                                                            STRAIN=C57BL/6; TISSUE=Duodenum; MEDLINE=98147142; PubMed=9486188; Yuan X., Zheng X., Lu D., Rubin D
                                                                                                                                                                                                                                                         Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                      Enteropeptidase (EC PRSS7 OR ENTK.
                                                                                                                                                                                                                                                                                                01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence up
28-FEB-2003 (Rel. 41, Last annotation
Enteropeptidase (EC 3.4.21.9) (Entero)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REPEAT
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REPEAT
                                                                                                                                                                                    Yuan X., Zheng X., Lu D., Rubin D.C., Pung C.Y.M., Sadl
                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                             NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                             01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Spermatogenesis;
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PTM: THE CHAINS ARE DERIVED FROM A SINGLE PRECURSOR CLEAVED BY A TRYPSIN-LIKE PROTEASE (BY SIMILARITY: BELONGS TO PEPTIDASE FAMILY SI.

SIMILARITY: Contains 2 LDL-receptor 71--SIMILARITY: Contains 2 LDL-receptor 71--
                                                                                    trypsinogen.
SUBUNIT: HETERODIMER
                                                                           MULTIDOMAIN (HEAVY)
                                                                                                                                                                                                                                                                                                                                                                                                   266 SPPENGLDKARGLKKDAPTSPASVASSSSTPSSKTKDL-GHNDKSST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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e splicing.
130
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558
771 AA;
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                                                                                                                                                                                                                                                                                                                   sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                        6;
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WD 2.
WD 3.
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WD 7.
PHOSPHORYLATION
PHOSPHORYLATION
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GLY/PRO-RICH.
CCN DOMAIN.
SER/PRO-RICH.
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• • • •
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 57.5;
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                                                                          CATALYTIC LINKED BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PHOSPHORYLATION
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                                                                                                                                                                                                                                                                                                 (Enterokinase)
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-> G (IN REF. 1).

-> R (IN REF. 2).
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CBC2)
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                                                                           BOND
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PÉAMI PEO0431 CUB; 2.

PÉAMI PEO0357; 1dl_recept_a; 2.

PÉAMI PEO1390; SEA; 1.

PÉAMI PEO1390; SEA; 1.

PÉAMI PEO1390; SRCR; 1.

PÉAMI PEO1390; SRCR; 1.

PÉAMI PEO0390; SRCR; 1.

PÉAMI PEO0390; LLLEGESTOR.

PRINTS; PRO0720; MAMDOWAIN.

PRINTS; PRO0721; LDLA; 2.

SWART; SM00102; LDLA; 2.

SWART; SM00102; SEA; 1.

SWART; SM00200; SEA; 1.

PROSITE; PS01180; CUB; 2.

PROSITE; PS01180; CUB; 2.

PROSITE; PS01040; MAM_2; 1.

PROSITE; PS00040; MAM_2; 1.

PROSITE; PS50060; MAM_2; 1.

PROSITE; PS50060; MAM_2; 1.

PROSITE; PS50040; SRCR_1; FALSE_NEG.

PROSITE; PS500420; SRCR_1; FALSE_NEG.

PROSITE; PS00134; TRYPSIN_HIS; 1.

PROSITE; PS00135; TRYPSIN_SER; 1.

PROSITE; PS00135; TRYPSIN_SER; 1.
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InterPro; IPR000859; CUB domain.
InterPro; IPR002172; LDL_receptor_A.
InterPro; IPR0001998; MAM_domain.
InterPro; IPR000098; MEM_domain.
InterPro; IPR001284; SEA_domain.
InterPro; IPR001294; Ser_protease_Try.
InterPro; IPR001196; Srcr_receptor.
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LDL-RECEPTOR CLASS A 2
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CHARGE RELAY SYS
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CYTOPLASMIC (POTENTIAL).
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Search completed: January 12, 2004, 14:24:51 Job time : 20 secs

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Q9pb60 xylella fas
O18118 caenorhabdi
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Q96kg7 homo sapien
Q9fkz9 arabidopsis
Q8g572 bifidobacte
Q8tb86 homo sapien
Q8ivf0 homo sapien
Q8ivf0 homo sapien
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Q91vi7 mus
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## ALIGNMENTS

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RESULT 1
Q93GH3
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Q93GH5
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Q93GH3;
Q1-DEC-2001 (TrEMBLrel. 19, Created)
Q1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
Q1-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical 6.2 kDa protein.
ERISB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (putative) lantibiotics, ericin A and ericin S."; Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases. EMBL; AF233755; AAL15569.1; -. Interpro; IPR000446; Nisin. PRINTS; PR00324; NISIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein. SEQUENCE 56 AA; 6241 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=A13;
Stein T., Borchert S., Conrad B., Feesche J., Entian K.-D.,
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Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hofemeister J.;
"A subtilin-like gene cluster of Bacillus subtilis Al3 encodes
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                                                                                                                                                                                                                                                                                                                                                                                                51.0%; Score 155; DB 2; Length 56; ilarity 54.7%; Pred. No. 8.2e-13; Conservative 10; Mismatches 12; Indels
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InterPro; IPR006078; Gallidermin.
InterPro; IPR006079; Lan dom.
Pfam; PF02052; Gallidermin; 1.
PRINTS; PR00323; GALLIDERMIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=22040717; PubMed=12044378;
Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Og
Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR006079; Lan dom.
InterPro; IPR000446; Nisin.
Pfam; PF02052; Gallidermin; 1.
PRINTS; PR00324; NISIN.
SEQUENCE 56 AA; 6195 MW; DI
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Bacteria; Firmicutes; Bacillales; Staphylococcus
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BSAA2 OR MW1765.
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EMBL; AF233755; AAL15567.1; -.
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01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                         acquired MRSA."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Yamamoto K., Hiramatsu K.; "Genome and virulence determinants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hofemeister J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lantibiotic ericin
                                                                                                                                                                                                                                                                                                                                                                                                                                ancet 359:1819-1827(2002).
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                                                                                                                                 KDFNLDL---VSVSKKDSGASPRITSTSLCTPGC-KTGA 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DFDLDVVKVSKQDSKITPQVLSKSLCTPGCITGPLQTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DENLDLVSVSKKDSGASPRITSTSLCTPGCKTGALMGC 42
                                                                                                        KVLDLDVQVKANNNSNDSAGDERITSHSLCTPGCAKTGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Borchert S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (TrEMBLrel.: (TrEMBLrel.:
  PRELIMINARY;
                                                                                                                                                                                             Conservative
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                                                                                                                                                                                        Score 77;
Pred. No.
5; Mismatc
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Last annotation update)
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Pred. No. 6.7e
6; Mismatches
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                                                                                                                                                                                                                                                                                 14715E32B0413532 CRC64;
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  PRT;
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  456
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9;
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Best Local S
Matches 14
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QBWUL3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001611; LRR.
InterPro; IPR007091; LRR_RNinh.
InterPro; IPR003590; LRR_RNinh_sub.
Pfam; PP00560; LRR; 3.
SWART; SW00368; LRR RI; 1.
PROSITE; PS50503; LRR RI; 4.
Hypothetical protein.
Hypothetical protein.
SEQUENCE 456 AA; 49816 MW; 007B78
                                                                                                                                                                                                                                                                                Pfam; PF00008; EGF; 8.

PRINTS; PR00011; EGFLAMININ.

SMART; SM00180; EGF Lam; 4.

PROSITE; P800022; EGF 1; 10.

PROSITE; P801186; EGF 2; 10.

EGF-like domain; Laminin EGF-like domain.

SEQUENCE 567 AA; 60797 MW; CF2FB8CDEB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Strausberg R.; Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases. EMBL; BC020198; AAH20198.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q91VI7;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR006209; EGF like.
InterPro; IPR002049; Laminin_EGF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases. EMBL; BC010331; AAH10331.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical RNH1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FISSUE=Muscle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MGD; MGI:1195456; Rnh1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FISSUE=Breast tumor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
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   149
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                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
   TSRCQ--CKNGAL--CNPITGACHCA 170
                                                                       TSLCTPGCKTGALMGCNMKTATCHCS 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 49.8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22.0%;
38.0%;
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                                                                                                                                        Score 63; DB 4
Pred. No. 9.2;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                               CF2FB8CDEB7CF627 CRC64;
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                                                                                                                                                                                                                Length 567,
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RESULT

Q96KG7 Q96KG7; Q1-DEC-2001

PRELIMINARY;

1140 AA.

01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19, 01-MAR-2003 (TrEMBLrel. 23,

Created)

update)

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RESULT 7
Q9FKZ9
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Best Local
 Matches
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                                                                      "Structural analysis of Arabidopsis thaliana chromosome 5. V. features of the regions of 1,381,565 bp covered by twenty one physically assigned Pl and TAC clones.";
DNA Res. 5:131-145(1998).
EMBL; AB010700; BAB08623.1; -.
InterPro; IPR006595; CTLH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AB058676; BAB47409.1; -.
InterPro; IPR006209; EGF like.
InterPro; IPR006209; EGF like.
InterPro; IPR002049; Laminin_EGF.
Pfam; PF00008; EGF; 14.
PRINTS; PR00011; EGFLAMININ.
SMART; SM00180; EGF_Lam; 6.
PROSITE; PS00022; EGF_1; 17.
PROSITE; PS01186; EGF_2; 17.
PROSITE; PS01186; EGF_2; 17.
Hypothetical protein; EGF-like domain; Laminin EGF-like domain.
SEQUENCE 1140 AA; 122204 MW; 45B2FA239423895A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-DEC-2001 (TrEMBLrel. 19, Last sequence update) 01-MAR-2003 (TrEMBLrel. 23, Last annotation updat MEGF10 protein (Hypothetical protein KIAA1780).
                                                                                                                                                                                                                                                  Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheop
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
                                                                                                                                                                                                                                                                                                    01-MAR-2001 (TrEMBLrel. 16,
01-MAR-2001 (TrEMBLrel. 16,
01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nagase T., Nakayama M., Nakajima D., Kikuno R., Ohara O., "Prediction of the coding sequences of unidentified human The complete sequences of 100 new cDNA clones from brain w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                       SEQUENCE FROM N.A. STRAIN=Columbia;
                                                                                                                                                                                                                                                                                         Gb | AAB71479.1 |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Hippocampus;
MEDLINE=21245130; PubMed=11347906;
                                                                                                                                                     Tabata S.;
                                                                                                                                                               Kaneko
                                                                                                                                                                          MEDLINE=98344145;
                                                                                                                                                                                                                          NCBI_TaxID=3702;
                                                                                                                                                                                                                                         eurosids II; Brassicales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
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             Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Res.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  large Proteins in vitro."; Res. 8:85-95(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                      149
                                               SM00668; CTL
VCE 752 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                             27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14;
                                                                                                                                                           T., Kotani
Similarity
20; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                      TSRCQ--CKNGAL--CNPITGACHCA 170
                                                                                                                                                                                                                                                                                                                                                                                                                                        TSLCTPGCKTGALMGCNMKTATCHCS
Conservative
                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                             CTLH;
                                                                                                                                                           Η.,
                                                                                                                                                             PubMed=9679202;
                                                 84436 MW;
          20.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20.7%;
                                                                                                                                                                                                                                        Brassicaceae;
                                                                                                                                                                                                                                                                                                     Created)
Last sequ
Last anno
Score 62; DB:
Pred. No. 17;
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
6,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 63; DB Pred. No. 19; 1; Mismatches
                                                 1FE23D5DC461AFC2 CRC64;
                                                                                                                                                                                                                                                                                                    annotation update)
                                                                                                                                                                                                                                                                                                                 sequence update)
                                                                                                                                                              Sato
                                                                                                                                                                                                                                                                                                                                                                                                                                            52
                                                                                                                                                                                                                                                                                                                                                        752
                                                                                                                                                           s:
                        DB 10;
                                                                                                                                                                                                                                        Arabidopsis
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                                                                                                                                                              Asamizu
21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1140;
                      Length 752;
 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                              Ε.
                                                                                                                                                                                                                                                               Tracheophyta;
                                                                                                                                                             Miyajima
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9
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Gaps
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2
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RESULT Q8IVF0

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RESULT ORGSTIC ORGSTIC
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Q8TBS6
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                                                                                                                                                 Matches
                                                                                                                                                                                    Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q8TBS6 PRELIMINARY; PRT; 536 AA.
Q8TBS6;
Q0TBS6;
Q1-JUN-2002 (TrEMBLrel. 21, Created)
O1-JUN-2002 (TrEMBLrel. 21, Last sequence update)
O1-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Similar to RIKEN CDNA 2610027L16 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "The genome sequence of Bifidobacterium longum reflects to the human gastrointestinal tract.";
Proc. Natl. Acad. Sci. U.S.A. 99:14422-14427(2002).
EMBL; AE014738; AAN24953.1; -.
Hydrolase; Complete proteome.
SEQUENCE 475 AA; 52701 MW; 2CF00D99B2F8C907 CRC64.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q8G572;
Q8G572;
                                                                                                                                                                                                                                                                                        EMBL; BC025332; AAH25332.1; -.
InterPro; IPR001313; Pumilio/Puf.
SEQUENCE 536 AA; 58248 MW; 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bifidobacterium longum.
Bacteria; Actinobacteria;
Bifidobacteriaceae; Bifid
                                                                                                                                                                                                                                                                                                                                                                                           Strausberg R.;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pessi G., Zwahlen M.-C., Desiere F., Pridmore R.D., Arigoni F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Deoxyguanosinetriphosphate triphosphohydrolase
DGT OR BL1148.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-2003
01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Lung;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
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Schell M.A., Karmirantzou M., Snel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           652
   100
                                                                     11 VSVSKKDSGASPRITSTSLCTPGCKTGALMGCNMKTATCH-CSIHV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11 VSVSKKDSGASPRITST-SLCTPGCKTGALMGCNMKTATCHCSIH
                                                                                                                                              l Similarity
13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SLKEVNTDLIGAIKSKSKKDSNTNLSSQVTTTSSSTMTSEDGGSSSLMMMTQT
LSTNRTGSEMLQELLGFSPLKPLCRVWAALRSNLRTVACHRCGVHV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STKDFNLDLV----SVSKKDSGA--SPRITSTSLCTPGCKTGALMGCNMKTAT
                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (TrEMBLrel.
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                                                                                                                                                                            20.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Primates;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20.2%;
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Desiere F., Bork P., Delle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Actinobacteridae; Bifidobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 61.5; D
Pred. No. 12;
8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8
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                                                                                                                                                                                    Score 61.5;
Pred. No. 1
                                                                                                                                                 Pred. No. 14;
); Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                               408722C248F2851C
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                                                                                                                                                                                                                          DВ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 16;
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                                                                                                                                                 23;
                                                                                                                                                                                                                                                                                                                                                                                                           databases
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                                                                                                                                                                                                                                                                                               CRC64;
                                                                                                                                                                                                                      Length
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                                                                        55
                                                                                                                                                                                                                          536;
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                                                                                                                                                 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1;
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RA Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Burandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Burandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Ballew R.M., Basu A., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Gorge N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local S
Matches 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-2000
01-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nagase T., Kikuno R., Ohara "The nucleotide sequence of Submitted (NOV-2002) to the EMBL; AB095941; BAC23117.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CG12908 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9V5J7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9V5J7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein NON_TER 1
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01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20.2%;
nilarity 28.3%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 648 AA;
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(TrEMBLrel.
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Primates; (
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el. 23, Last sequence update)
el. 23, Last annotation updat
KIAA2021 (Fragment).
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23,
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a long cDNA clone
EMBL/GenBank/DDBJ
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Pred. No. 17;
9; Mismatches
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Celniker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,

A Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,

A Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,

A Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,

A Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,

A Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,

A Perriera S., Frise E., Galle R.F., Garg N.S., George R.A.,

A Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,

A Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,

A McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunco J.,

A McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunco J.,

A McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunco J.,

A Pacleb J., Paraggas V., Park S., Patel S., Pfeiffer B.,

A Phouanenavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,

Stapleton M., Strong R., Svirskas R., Tector C., Tyler D.,

Milliams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;

"Sequencing of Drosophila melanogaster genome.";

Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                         FlyBase; FBgn0033509; CG12908.
InterPro; IPR000152; Asx_hydroxyl.
InterPro; IPR00181; EGF Ca.
InterPro; IPR006209; EGF_like.
InterPro; IPR006210; IEGF.
InterPro; IPR00033; Ldl_receptor_rep.
InterPro; IPR00386; Nidogen_ext.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM ACCORDANCE SAdams M.D., Celniker S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

Miera S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campyonia S., Crosby M.A., Matthews B.B., Prochnik S.E., Smith C.D., Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Celniker S.E., Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E., Tupy J.L., Drysdale R., Emmert D., Frise E., de Grey A., Harris N., Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N., Kronmiller B., Marshall B., Millburn G., Richter J., Russo S., Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E., Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E., Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E., "Annotation of Drosophila melanogaster genome.";

"Annotation of Drosophila melanogaster genome.";

"Annotation of Drosophila melanogaster genome.";
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Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
Syirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
Zheng X.H., Zhong F.N., Zhong W., Zhou S., Zhu X., Smith H.O.,
Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
"The genome sequence of Drosophila melanogaster.";
Science 287:2185-2195(2000).
                 PROSITE;
PROSITE;
PROSITE;
EGF-like
                                                                                                     Pfam; PF00008; EGF; 6.
Pfam; PF00058; Idl recept b; 2.
SMART; SM00131; EFF; 11.
SMART; SM00135; LY; 4.
SMART; SM00539; NIDO; 1.
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                                                                                                                                                                                                                                                                                                                                                                                      Submitted (SEP-2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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domain.
1350
                                     PS00010; ASX_HYDROXYL;
PS01186; EGF_2; 9.
PS01187; EGF_CA; 1.
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                                                                                                                                                                                                                                                                                                                                                                                        EMBL/GenBank/DDBJ databases
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482243B79347A341
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Reese M.G.,
Chen H.,
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Query Match Best Local S Matches 12

Similarity 12; Conserv

Conservative

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Pred. No. 42; 3; Mismatches

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       Matches
                                                               Query Match
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Q924P4;
Q1-DEC-2001
Q1-DEC-2001
Q1-MAR-2003
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01-JUN-2002
01-OCT-2002
                                                                                                                                                                                                                                                                                           Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Champe M., Chavez C., Dorsett V., Dresnek D., Frian D., Friae George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last seq
01-MAR-2003 (TrEMBLrel. 23, Last ann
Ribonuclease/angiogenesis inhibitor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
Stapleton M., Brokstein P.,
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                                                                                                                                                                                                    Submitted (JAN-2002) to the EMBL/GenBank/DDBJ EMBL; AY075166; AAL68036.1; -.
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InterPro; IPR007091; LRR_RNinh.
InterPro; IPR003590; LRR_RNinh_sub.
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                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                          Celniker S.;
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; SM00368; LRR RI; 1.
; FS50503; LRR RI; 4.
;NCE 456 AA; 49626 MW;
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       l Similarity
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773 AA; 8:
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                                                                                                                                     84788
                                   19.7%;
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Pred. No. 18;
7; Mismatches
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                                                                                                                                     080468E1D601FCDF CRC64,
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                                                                  DB 5; Length 773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     B
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   16;
                                                                                                                                                                                                                                       databases
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       Indels
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RESULT OF THE SOLE OF THE SOLE
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RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Galle R.F.,
RA Amanatides P.G., Scherer S.E., Holt R.A., W., Honderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Haris M.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Ffannkoch C., Baldwin D.,
RA Ballew R.M., Besu A., Baxendale J., Bayrakkaroglu L., Beasley E.M.,
RA Beson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Gherry J.M., Cayley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cayley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cayley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cayley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cayley S., Dahlke C., Perraz C., Ferriera S., Fleischmann W.,
RA Cherry J.M., Cayley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cayley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cayley S., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Cherry J.M., Cayley S., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Cherry J.M., Cayley S., Downes M., Dugan-Rocha S., Fleischmann W.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Howland T.J., Wei M.-H., Ibegwam C.,
RA Kimmel B.E., Kodira C.D., Kraft C., Krevitz S., Kull D., Lai Z.,
Lin X., Mattei B., McDincoh T.C., McLeod M.P., McPherson D.,
RA McInlov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Melson D.R., Nelson K.A., Saunders R.D.C., Scheeler F., Shen H.,
RA Melson D.R., Nelson K.A., Saunders R.D.C., Scheeler F., Shen H.,
RA Melson D.R., Nelson K.A., Shuph M., Nelson D.A.,
RA Mang S.-Y., Massarman D.A., Weinstock
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              밁
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01-MAR-2003 (Tran
CG14982 protein.
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Q9VZK7;
SEQUENCE FROM N.A.

Gelniker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A., Celniker S.E., Adams M.D., Amanatides P.G., Brandon R.C., Rogers Y., Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Busam D.A., Carlson J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A., Carlson J., Center A., Champe M., Davenport L.B., Dietz S.M., Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D., Ferriera S., Frise E., Galle R.F., Garg N.S., George R.A., Ferriera S., Frise E., Galle R.F., Hostin D., Howland T.J., Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J., Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A., McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunco J., Paragas V., Park S., Patel S., Pfeiffer B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CG14982
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NCBI_TaxID=7227;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophilidae; Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PubMed=10731132;
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Last sequence update)
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RESULT 15
Q9PB60
         A CONTRACTOR OF THE CONTRACTOR
                  A Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M.,
A Alvarenga R., Alves L.M.C., Arruda P., Baia G.S., Baptista C.S.,
A Alvarenga R., Alves L.M.C., Brodin S., Bove J.M., Briones M.R.S.,
A Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,
A Colauto N.B., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrer H.,
A Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,
A Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorry H.,
A Facincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,
A Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,
A Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
A Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Kitajima J.P.,
A Hop L.L., Hoheisel J.D., Jungueira M.L., Kemper E.L., Kitajima J.P.,
A Krieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,
A Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,
A Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.L.,
A Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
A Mench C.F.M., Miracca B.C., Miyaki C.Y., Monteiro Vitorello C.B.,
A Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
A Monni A. Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,
B Marcia B.C., de Oliveira R.C., Palnieri D.A., Paris A.,
Coliveira M.C., Paris A., Paris A.,
Coliveira M.C., Paris A., Paris A.,
Coliveira M.C., Paris A.,
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Best Local S
Matches 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FlyBase;
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D., Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E., Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N., Kronmiller B., Marshall B., Millburn G., Richter J., Russo S., Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E., Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E., "Annotation of Drosophila melanogaster genome.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; Xylella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical XF2284.
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01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-OCT-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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Submitted (MAR-2000) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Phouanenavong
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FBgn0035477; CG14982.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LVAATRRDSGSSTQHSANSYCGYVTPAGDYSGMGGGRNTECLDCRC 502
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (TrEMBLrel. 15, TrEMBLrel. 15, TrEMBLrel. 20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein
            Pereira
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19.7%;
      G.A.G., Pereira H.A. Jr.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E., Gibbs R.A., Rubin G.M., Vente
the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 60,
Pred. No.
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                                                                                                                            EMBL; AE004040; AAF85083.1; -. Hypothetical protein; Complete SEQUENCE 78 AA; 8776 MW; 10
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Search completed: January 12, 2004, 14:25:56 Job time: 56 secs

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## ALIGNMENTS

TITLE	AUTHORS	REFERENCE			ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION	DEFINITION	LOCUS	STRSPAN	RESULT 1
Structure, expression, and evolution of a gene encoding the precursor of nisin, a small protein antibiotic	Buchman, G.W., Banerjee, S. and Hansen, J.N.	1 (bases 1 to 767)	Lactococcus.	Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;	Lactococcus lactis	Lactococcus lactis	nisin; small protein antibiotic.	J04057.1 GI:153816	J04057	S.lactis antibiotic nisin (spaN) gene, complete cds.	STRSPAN 767 bp DNA linear BCT 15-FEB-1996		

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AF465351
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Submitted (05-JAN-2002) Department of Dairy and
Royal Veterinary and Agricultural University of
Rolighedsvej 30, Frederiksberg C 1958, Denmark
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 2467)
Johansen, A.H., Vogen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AATATACTCAAGTCATTGAGACTGTAAGTAAAATAAAGTTTTTTTGGAACAGTTACTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTCAACCGTTTTTAGTAAGAAATACAATTTTATCTCCAAACGATAAACGGAGTTTTACTG
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                                                                                                                                                                                                                                                                                                                      db xref="taxon:1358"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Vogensen, F.K. and Jelle, B
                                                                                                                                                                                                                                                                                                      obtained
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                     TAGCTAATCCTAAACTCTATGATGTTATGCAGAAATATAATGCTGGT 767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGATACAATGATTTCGTTCGAAGGAACTACAAAATAAATTATAAAGGAGGCACTCAAAATG
                                                                                         AATATACTCAAGTCATTGAGACTGTAAGTAAAAATAAAGTTTTTTTGGAACAGTTACTAC
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                                                                                                                                                                                                                                                                                                                             AGGATAGTATTTTGTTAGTTCAGACATGGATACTATCCTATTTTTATAAGTTATTTAGGG
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LDDYKDKFIEKYGVDQEVQITELFDSTFGIGAVD"

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Pred. No. 9.8e-123;
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        121
                                                                                                               448
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (17-SEP-2001) Division of Applied Life Science, Gyeongsamg National University, 900 Gaja-dong, Jinju, Gyeongnam
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lee, K.-H., An, J.-Y., Yun, H.-D., Lee, H.-J., Chung, D.-K., Lee, J.-H. and Kim, J.-H. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 1575)

Lee, K.-H., An,J.-Y., Yun,H.-D., Lee,H.-J.,

Chung,D.-K., Lee,J.-H. and Kim,J.-H.

Characterization of a nisin-producing Lacto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene, partial cds.
AF420259
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Bacteria; Fírmicutes; Lactobacillales;
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                                                                                                                                                                                                 Similarity
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                                                                    GAGATAGGTTTATTGAGTCTTAGACATACTTGAATGACCTAGTCTTATAACTATACTGAC
                                                                                                                                 AGTTGACGAATATTTAATAATTATTAATATCTTGATTTCCTAGTTCCTGAATAATATA 60
        AATAGAAACATTAACAAATCTAAAACAGTCTTAATTCTATCTTGAGAAAGTATTGGTAAT
                                                                                                               AGTTGACGAATATTTAATAATTTAATATATCTTGATTTTCTAGTTCCTGAATAATATA
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                                                                                                                                                                                                                                                                      590
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INSSELEEVNIKYTNVQGISEF"
INSSELEEVNIKYTNVQGISEF"
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198 c 257 g 530 t
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                                                                                                                                                                                Score 765.4; DB 1;
Pred. No. 2e-122;
0; Mismatches 1;
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and NisB (nisB)
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Lactococcus lactis
Bacteria; Firmicutes; Lactobacillales;
                                                                                                                                                                                    Nutritional Science Laboratory
Morinaga Milk Industry Co., Ltd.
1-83, 5 Higashihara
                                                                                                                                                                                                                                                       These data kindly submitted in
                                                                                                                                                                                                                                                                          Unpublished
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81-462-52-3055
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71. .109
                                                                                                    Location/Qualifiers
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                                  mol_type="genomic DNA"
strain="NCDO497"
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/transl_table=11
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/note="ORF3"
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QLLLANPKLYDVMQKYNAGLLKKKRVKKLFESIYKYYKRSYLRS"
415 c 478 g 848 t
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DQSQYTSSRYQSTLRQVGAQSSMSRKGNPYDNAMMESFYKTLKRELINDAHFETRAE
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/transl_table=:
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                                                                              Direct Submission
Direct Submission
Submitted (07-SEP-1992) G. Engelke, Inst. fuer Mikrobiologie,
Submitted (07-SEP-1992) Theodor-Stern-Kai 7, Haus 75A, 6
                                                                                                                                                                                               Engelke, G., Gutowski-Eckel, Z., Hammelmann, M. and Entian, K.D. Biosynthesis of the lantibiotic nistn: genomic organization membrane localization of the NisB protein Appl. Environ. Microbiol. 58 (11), 3730-3743 (1992)
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X68307.1 GI:44040
biosynthetic enzyme; lantibiotic; nisZ
Lactococcus lactis
Lactococcus lactis
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biosynthetic enzymes.
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BASE COUNT
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nilarity 99.5%;
Conservative
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YDDLKIILIINFLSNLTKENNGLISLYIKSENQMSQSESEMYPLGCLNMGLAHGLAGVG
YDDLKIILIINFLSNLTKENNGLISLYIKSENQMSQSESEMYPLGCLNMGLAHGLAGVG
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GLIEICSLFKRLLNTKKFDSYMEEFNVNSEQILEEYGDESGTGFLEGISGCILVLSKF
EYSINTYWRQALLLFDDFLKGGKRK"
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FFKKASIYILDEPSAALDPVAEKEI FDYFVALSENNI SI FI SHSLNAARKANKI VVMK
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/gene="nisC"
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Pred. No. 6.1e-120;
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Direct Submission
Submitted (07-DEC-1992) Immonen T., I
Submitted no. Do. Box 56, FIN-00014,
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Engelke,G., Gutowski-Eckel,Z., Hammelmann,M. and Entian,K.D.
Biosynthesis of the lantibiotic nisin: genomic organization
membrane localization of the NisB protein
Appl. Environ. Microbiol. 58 (11), 3730-3743 (1992)
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Immonen, T., Ye, S., Ra, R., Qiao, M., Paulin, L. and Saris, P.E.
The codon usage of the nisz operon in Lactococcus lactis N8
suggests a non-lactococcal origin of the conjugative nisin-sucrose
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gene; nisZ gene.
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                                                                                                                                                                           /gene="nisB"
520..3501
                                                                                                                                                                                                                           KTATCNCSIHVSK"
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239. .412
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                organism="Lactococcus"
/mol type="genomic DNA"
                                                                                                                                                                                                                                             translation="MSTKDFNLDLVSVSKKDSGASPRITSISLCTPGCKTGALMGCNM
                                                                                                                                                                                                                                                                                                                                                                citation=[1]
                                                                                                                                                                                                                                                                                                                                                                                                gene="nisin"
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                                                                                                                                                                                                                                                                                                                                                                                  function="antibiotic"
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University of Helsinki,
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GLLEICSLERRLLNTKKFDSYIEEFNUNSEQILEEYGDESGTGFLEGISGCILVLSKF
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YSINNRLMRTTSSLELSDYEQADMYNIIEKVTQDSTYKFFQLFNAIIVVLSSFISLLS
SLFFIGTWNIGVAILLLIVPULSLVLFLRVGQLEFLIQWQRASSERETWYIVYLLTHD
FSFKEIKLNNISNYFIHKFGKLKKGFINQDLAIAKKTYVINIFLDFILNILTIIA
MILSVRAGKLLIGUNVSLIQALSKINTYSQTMLQNIYIIYNTSLFMEQLFEFKRESV
VHKKIEDTEICNQDIGTVKVINLSYVYPNSNAFALKNINLSFEKGELAAIVGKNGSGK
STLVKIISGLYQPTMGJIQYDKWRNSLMPEEFYQKNISVLFQDFVKYELTIRENIGLS
DLSSQWEDEKIIKVLDNIGLDFLKTNNQYVLDTQLGNWFQEGRQLSGGQWKIALART
FFKKASIYILDEPSAALDFVAEKEIFDYFVALSENNISIFISHSLNAARKANKIVVMK
DGQVEDVGSHDVLLRRCQYYQELYYSEQYEDNDE"
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DIVGNINILGGASGRFSALSPELTSYHRTIVDSYERENENKEITSCEIVFLEBIRHAN
VMHTSIMRRKVLPFFTSTSHNEVQLTNIYIDEBEKFKPAISTGEVLKFYITSMYN
KTLFSNELFFLXEISLDDKFGNLPWELLYRDFDYIPRLVFDEIVISPAKKKIWGRDVN
KMTIRELIQSKEIFKEFYIVNDDNKVYLSQENPLDMEILESAIKKSSKRKDFIELQE
YFEDENIINKGQKGRVADVVVPFIRTRALGNEGRAFIREKRSVERREKLFPLEMLYL
KLYISINRQNEFLLSYLPDIQKIVANLGKEFPETLRYDDFHIRLT KGSDLFLAYGS
ILEILKRSQKNRIMSTFDISIVQGEVERYGGFDTLELSEAIFCADSKIIPNLTTLIKD
TNNDMKVDDVSILVNYLYLKCFFQNDNKKILNFLNLVSFKVKENVNEKIEHYLKLLK
VDNLGDQIFYDSMFKELKHAIKNLFLKMIAQDFELQKVYSIIDSIIHVHNNRLIGIER
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INSSELEEVNIKYTNVYQIISECENDYQKYEDISETVTLCYGDFYELSEQYLGSLI
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YFVTDKEIPQENVNNCKVKFYNLLIVDMKSEKLLSSSNKNSVTLVLNNIYEASDKSLC
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                                                                                   ACTAGCTAATCCTAAACTCTATGATGTTATGCAGAAATATAATGCTGGT
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/db_xref="GI:581294"
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/translation="MKKILGFUFUCSIGLSATVHGETTNSQOLLSNNINTELINHNS
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DTTVSDEELGEYQDVLAEVRVFDSVSGKSIPRSEWGRIDKDGSNSKQSRTEWDYGEIH
SIRGKSLTEAFAVEINDDFKLATKVGN"
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citation=[1] citation=[2] 'gene="nisC"

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359 418 358

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3512

DKEKLIYYTLQRLFVSEEYMK"

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Gaps

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EYSINFTYWRQALLLFDDFLKGGKRK"

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/codon\_start=1 /transl\_table=11 citation=[1]

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Gasson, M.J. and Dodd, H.M.
Production of variant nisin
Patent: US 6448034-A 29 10-SEP-2002;
Location/Qualifiers
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Sequence
AR228341
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                  AAATATAATGCTGGT 767
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                                                                                                                                   AAAAACATGATAAAAAGTTCATTTAAAGCTCAACCGTTTTTAGTAAGAAATACAATTTTA
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29 from patent US 6448034.
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LACNISABTC
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Kuipers,O.P., Beerthuyzen,M.M., Siezen,R.J. and De Vos,W.M. Characterization of the nisin gene cluster nisABTCIPR of Lactococcus lactis. Requirement of expression of the nisA genes for development of immunity

Eur. J. Biochem. 216 (1), 281-291 (1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nisA gene; nisB gene;
translocator protein.
Lactococcus lactis
Lactococcus lactis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 L16226.1 GI:400365
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                                                            LDDYKDKFIEKYGVDQEVQITELFDSTFGIGAPYNYNHPRNDFYESEPSTLYYSEEER
EKYLSMYVEAVKNHAVINLDDLESHYQKMDLEKKSELQELELFULLAKEYEKDIFILG
DIVGNNLGGASGRFSALSPELTSYHRTIVDSVERENENKEITSCEIVFLPENIRHAN
VMHTSIMRRKYLPFFTSTSHBEVLLTNIY1GIDEKEKFYARDISTQEVLKFYITSMYN
KTLFSNELFLYEISLDKFGNLPWELIYRDFDYIPRLVFDEIVISPAKWKIWGRDVN
SKMTLRELIQSKEIPKEFYIVNGDNKYVLSQENPLDWEILSSAIKKSSKRKDFIELQE
YFEDENIINKGEKGRVADVVVPFIRTRALGNEGRAFKEVSVERRKEKLPPNEWLYL
KLYISINRQNEFLLSYLDDIQKIVALGGNLFFLRYTDFKHIRLRIKGSDLFLAYGS
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TNNDWKVDDVSILVNYLYLKOFFQNDNKKILNFLNLVSPKKVKENNNEKIEHYLKLK
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INSSELEEVNIKYTOTOSECENDYKYEDICETYTLCYGDEYRBLSEQYLGSLI
VNHYLISHLQKDLLSDFSWNTFLTKYBAIDEDKKYIIPLKKVOKFIQEYSEIBIGEGI
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                                             VNNLGDQ1FYDKNFKELKHA1KNLFLKM1AQDFELQKVYS11DS11HVHNNRL1G1EF
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/strain="NIZO R5"
/sub_species="lactis"
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protein id="AAA25189.1"
db_xref="GI:400366"
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'transl_table=
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ACAATGATTTCGTTCGAAGGAACTACAAAATAAATTATAAGGAGGCACTCAAAATGAGTA 180
                                 ACAATGATTTCGTTCGAAGGAACTACAAAATAAATTATAAGGAGGCACTCAAAATGAGTA 304
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/db_xref="GI:400368"
/db_xref="GI:400368"
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SLFFIGTMNIGVAILLLIVPVLSLVLFILVATUGQLEFILQWQRASSERETMYIVYLLTHD
FSFKEIKLNNISNYFTHKFGKLKKGFINQDLALARKKTYFNIFLDFILMLINILTIFA
MILSVRAGKILLIGNLVSLIQALSKINTYSQTMIQNIYIIYNTSLFMEQLFEFLKRESV
VHKKIEDTEICNQHIGTVKVINLSVLAGARAFLKNINLSFEKGELTALVGKNGSGK
STLVKIISGLVQPTMGIIQVDALSKINTYSQTMIQNISVLFQDFVXSLTTRENIGLS
DLSSQWEDEKIIKVLDNLGLDFLKTNNQYVLDTQLMWFQEGHQLSGGQWQKIALART
FFKKASIYILDEPSAALDPVLEKEIFDYFVALSENNISIFISHSLNAARKANKIVVMK
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/transl_table=1
/label=ORF
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/db_xref="GI:400370"
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/db_xref="GI:400369"
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Sequence 1 from Patent WO9941978.
AX002982
                                                                                                                                                                                                                                                                                                                                                                                                                             Performance enhancement
Patent: WO 9941978-A 1 26-AUG-1999;
FLANAGAN ALISON JOHNSTONE (GB); ROLPH TIMOTHY PETER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lactobacillus delbrueckii subsp. lactis
Lactobacillus delbrueckii subsp. lactis
Bacteria; Firmicutes; Lactobacillales;
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a 913 c
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/sub_species="lactis"
/db_xref="taxon:29397"
/note="NIZO R5"
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83.8%; Score 643; DB 6;
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tive 0; Mismatches
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N L.lactis ORF1 and ORF2 (nisin) gene, comp
gene, 5' end.
M79445
M79445.1 GI:149451
nisin.
Lactococcus lactis
M Lactococcus lactis
Bacteria; Firmicutes; Lactobacillales; St
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J. Gen. Microbiol. 136 (Pt 3), 555-5
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Location/Qualifiers
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625. .1386
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larity 100.0%;
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Mintrkryklavaidyakgsrykykhynkgaslsrenlinglykatarapkkvmlgdm
Tylptkegtilavaidyesbkivgksmsskydklyrdcfloacgkehpqpglivh
DQGSQYTSSRYQSTLRQVGAQSSMSRKGNPYDNAMMESFYKTLKRELINDAHFETRAE
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391 c 450 g 78
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/db_xref="GI:551876"
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/protein_id="AAA25197.1"
/db_xref="GI:149452"
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'protein id="AAA25198.1"
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'translation="MSTKDFNLDLVSVSKKDSGASPRITSISLCTPGCKTGALMGCNM
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Pred. No. 1.1e-94;
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PAT 02-DEC-1994

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UNIVERSITY OF MARYLAND
OS Bacillus subtilis
PN JP 2002191383-A/2
PD 09-JUL-2002
PF 08-NOV-2001 JP 2001343857
PR 05-JUL-1988 US 214959
PI NORMAN J HANSEN 214959
PI NORMAN J HANSEN 21495
PC C12N15/09_CO7K14/195_C12N15/00
CC Leader sequence inducing a post-translational modification of CC in bacteria, and gene therefor FH Key Location/Qualifiers
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BD166172
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JP 2002191383-A/2.
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                                                                                                AGATACAATGATTTCGTTCGAAGGAACTACAAAATAAATTATAAAGGAGGCACTCAAAATG
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CCACGCATTACAAGTATTTCGCTATGTACACCCGGTTGTAAAACAGGAGCTCTGATGGGT
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LEADER SEQUENCE INDUCING A POST-TRANSLATIONAL MODIFICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unclassified
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                               AGGATAGTATTTTGTTAGTTCAGACATGGATACTATCC 518
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                                                                  TGTAACATGAAAACAGCAACTTGTCATTGTAGTATTCACGTAAGCAAATAACCAAATCAA
                                                                               TGTAACATGAAAACAGCAACTTGTCATTGTAGTATTCACGTAAGCAAATAACCAAATCAA
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              AGGATAGTATTTTGTTAGTTCAGACATGGATACTATCC
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Submitted (02-APR-2002) Sang-Hee Park, Tokyo University, Laboratory Submitted (02-APR-2002) Sang-Hee Park, Tokyo University, Laboratory of Veterinary Public Health; Bunkyouku yayoi 1-1-1, Tokyo 113-8657, Japan (E-mail:park3hee@hotmail.com, Tel:81-3-5841-5476,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Curr.
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Park, S.H.
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Lactococcus lactis subsp. lactis
Bacteria; Firmicutes; Lactobacillales;
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Identification and Characteristics of Nisin Z-Producing Lactococcus
Lactis subsp. lactis Isolated from Kimchi
Curr. Mcrobiol. 46 (5), 385-388 (2003)
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                                                                                                                                                                                        303
                                                                                                                 Conservative
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                                                                                                                                                                                                                                             /Codon_start=1
/transI_table=11
/product="nisin_B"
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QLLLANPKLYNVMQKYNAGLIKKKKVKKLFESIYKYYKRSYLRSTPFGLFSETSIGVF
SKSSOYKLMGKTTKGIRLDTOMLIKHKMEVDFSKKLSFTRNNANYKFGDRVFQVY"
99 C 141 g 253 t
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                                                                                                                                                                                                                                                                                                                                                                                           /protein_id="BAC20309.1"
/db_xref="GI:23496477"
/translation="MSTKDFNLDLVSVSKKDSGASPRITSISLCTPGCKTGALMGCNM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Lactococcus lactis subsp.
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/transī_table=11
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/sub_species="lactis"
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Pred. No. 3.2e
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Steen,M.T., Chung,Y.J. and Hansen,J.N.
Characterization of the nisin gene as part of a polycistronic operon in the chromosome of Lactococcus lactis ATCC 11454
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                                                                                                                                                                                                                                                                                                                                                                                                    Original source text: Lactococcus Location/Qualifiers
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Bacteria; Firmicutes;
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Lactococcus lactis
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                                                                                                                                       KTATCHCSIHVSK"
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transl_table=
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                                                                                                                                                           translation="MSTKDFNLDLVSVSKKDSGASPRITSISLCTPGCKTGALMGCNM/
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                                                                                                                                                                                                                                                                                                                                 mol_type="genomic DNA"
db_xref="taxon:1358"
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RESULT 15
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-10_signal
-35_signal
-10_signal
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  LLLINISZ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGTTGTAACATGAAAACAGCAACTTGTCATTGTAGTATTCACGTAAGCAAATAACCAAAT 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TCACCACGCATTACAAGTATTTCGCTATGTACACCCGGTTGTAAAACAGGAGCTCTGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TACTAGCTAATCCTAAACTCTATGATGTTATGCAGAAATATATAATGCTGGT 767
                                                                                                                                                                                                                              CTGAATATACTCAAGTCATTGAGACTGTAAAGTAAAAATTAAAGTTTTTTTGGAACAGTTAC
                                                                                                                                                                                                                                                                                                                                                                                                GGGTTGCTAAATAGCTTATAAAAATAAAGAGAGAGAAAAAACATGATAAAAAGTTCATTTA 597
                                                                                                                                                                                                                                                                                                                                                                                                                                                          CAAAGGATAGTATTTTGTTAGTTCAGACATGGATACTATCCTATTTTTATAAGTTATTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TCACCACGCATTACAAGTATTTCGCTATGTACACCCGGTTGTAAAACAGGAGCTCTGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTGAATATACTCAAGTCATTGAGACTGTAAGTAAAAATAAAGTTTTTTTGGAACAGTTAC
                                                                                                                                                                                                                                                                                    AAGCTCAACCGTTTTTAGTAAGAAATACAATTTTATCTCCAAACGATAAACGGAGTTTTA
                                                                                                                                                                                                                                                                                                          AAGCTCAACCGTTTTTAGTAAGAAATACAATTTTATCTCCCAAACGATAAACGGAGTTTTA
                                                                                                                                                                                                                                                                                                                                                                     GGGTTGCTAAATAGCTTATAAAAATAAAGAGAGGAAAAAAACATGATAAAAAGTTCATTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAAAGGATAGTATTTTGTTAGTTCAGACATGGATACTATCCTATTTTTATAAGTTATTTA 537
                                                                                                              TACTAGCTAATCCTAAACTCTATGATGTTATGCAGAAATATAATGCTGGT
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LDDYKKFIEKKGVDQEYQITELFDSTFGIGA FYNYNHERNDFYESEBSTLYYSSEER
EKYLSMYVEAVKONHNU HUDDLESHYQOMDLEKKSELQFLEIFUNLAKEYEDIFILG
DIVGNNNLGGASGRFSALSPELTSYHRTIVDS VERENENEITSCEIVFLEENIRHAN
VMHTSIMERKYLLFFFTSTSHNEVLLTNIYIGIDEKEKFYARDISTQEVLKFYITSMYN
KTLFSNELRFLYEISLDDKFGNLFMELIYEDFDIFILFDEIVISPAKWKIMGRDVN
KTHESNELRFLYEISLDDKFGNLFMELIYNDFDIFRTEALGERENENEILSAIKKSSKRKDFTIELGE
YFEDENIINKGEKGRVADVVVPFIRTRALGNEGRAFIEKRVSVERREKLFFNEMLYL
YFEDENIINKGEKGRVADVVVPFIRTRALGNEGRAFIEKRVSVERREKLFFNEMLYL
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INSSELEEVNIKYTNVYQIISEFCENDYQKYEDICETVTLCYGDEYRELSEQYLGSLI
VNHYLISNLQKDLLSDFSWNTFLTKVEAIDEDKKYIIFLKKVQKFIQEYSEIEIGEGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /protein_id="AAA73040.1"
/db_xref="GI:149450"
/translation="MDEVKEF"
383 c 590 g 1053
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QLLLANPKLYDVMQKYNAGLLKKKRVKKLFESIYKYYKRSYLRSTPFGLFSETSIGVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KLYISINRQNEFILLSYLPDIQKIVANLGGNLFFLRYTDPKPHIRLRIKCSDLFLAYGS
ILEILKRSRKNRIMSTFDISIYDQEVERYGGFDTLELSEAIFVPILKLFQICLH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              codon_start=1/transl_table=
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Query Match
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Pocus

2778

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DNA

linear

BCT 27-OCT-1999

59.0%;

Score 452.6;

DB ۲.

Length 2778;

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BASE COUNT
ORIGIN
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AUTHORS
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AUTHORS
TITLE
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KEYWORDS
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PUBMED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (27-MAY-1997) T. Immonen, Institute Of Biotechnology,
Biocenter 1, Viikinkaari 9, P.O.Box 56, 00014 University Of
Helsinki, FINLAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lactococcus lactis subsp. lactis
Lactococcus lactis subsp. lactis
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99452384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA Seq. 9 (5-6), 245-261 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Immonen, T., Wahlstrom, G., Takala, T. and Saris, P.E. Evidence for a mosaic structure of the Tn5481 in Lactococcus lactis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nisin Z; NisZ gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Immonen, T
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                       1020
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                                         /trānslation="MSTKDFNLDLVSVSKKDSGASPRITSISLCTPGCKTGALMGCNM
KTATCNCSIHVSK"
                                                                                                                                                                                                                                                      2605
                                                                                                                                                                                                                                                                     /db¯xref="SPTREMBL:069439"
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VRGNPLVFEYSRKPWIIPDNGDVASNQSVINRCPSGALKYLAKEKN"
                                                                                                                                                                                                                                                                                                                                                                                                                                           complement (932. .1204)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /trānslation="MPFWSTKIFGEGEKLMNIIERENLFELLSDKGEIIGEMAYMPMN
NSIIITHTGVSLDYRGQGLAKKLVLAGIQKARREQLKLGATCPYAVKYFREHKEELTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="MEEKLAGKDYLFIGSMLFGLFFGAGNLIFPIHMGQEAGAAISQA
NFGFLITAVGFPFLGIIALGISQSNGVFELASRVNRIYAYIFTILLYLVIGPFFALPR
LATTSFEIGISPFLSHELQAPLLALFSILFFGTAWFLSR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /producT="homologous to branched chain amino acid
transporters of LIV-II class"
/protein_id="CAA73811.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(<1. .423)
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/transi_table=11</pre>
                                                                                                                                                                                                                                                                                                                           /product="YjdI-like protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="YjdJ-like protein"
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/db_xref="GI:3157418"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement (660. .977)
                                                                                                                                                                                       2605. .2778
/gene="nisZ"
                                                                                                                                                                                                                                                                                                                                                                                                 /codon_start=1
/transl_table=
                                                                                  protein_id="CAA73814.1"
/db_xref="GI:3157420"
                                                                                                                       product="nisin Z"
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/clone="pLEB506"
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                       923
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Best Lo Matches	cal Similarity 98.9%; 466; Conservative 0	Pred. No. 1.3e-68; ; Mismatches 4; Indels 1; Gaps 1;
\$	1 AGTTGACGAATATTTAATAA:	AGTTGACGAATATTTAATAATTATTAATATCTTGATTTCTAGTTCCTGAATAATATATA 60
DЪ	2309 AGTTGACGAATATTTAATAA	AGTTGACGAATATTTAATAATTTATTAATATATCTTGATTTTCTAGTTCCTGAATAATATATA 2368
Ş	61 GAGATAGGTTTATTGAGTCT	GAGATAGGTTTATTGAGTCTTAGACATACTTGAATGACCTAGTCTTATAACTATACTGAC 120
망	2369 GATATAGGTTTATTGAGTCT	GATATAGGTTTATTGAGTCTTAGACATACTTGAATGACCTAGTCTTATAACTATACTGAC 2428
Ş	121 AATAGAAACATTAACAAATC	AATAGAAACATTAACAAATCTAAAAACAGTCTTAATTCTATCTTGAGAAAGTATTGGTAAT 180
дb	2429 AATAGAAACATTAACAAATCTAAAACAGTCTTAA	TAAAACAGTCTTAAITCTATCTTGAGAAAGTATTGGCAAT 2488
γ	181 AATATTATTGTCGATAACGCC	AATATTATTGTCGATAACGCGAGCATAATAAACGGCTCTGATTAAATTCTGAAGTTTTGTT 240
90	2489 AATATTATTGTCGATAACGCC	AATATTATTGTCGATAACGCGATCATAATAAACGGCTCTGATTAAATTCTGAAGTTTGTT 2548
Q.	241 AGATACAATGATTTCGTTCG	AGATACAATGATTTCGTTCGAAGGAACTACAAAATAAATTATAAGGAGGCACTCAAAATG 300
Ф	2549 AGATACAATGATTTCGTTCGAAGGAACTAC-	AAGGAACTAC-AAATAAATTATAAGGAGGCACTCAAAATG 2607
ઇ	301 AGTACAAAAGATTTTAACTT	AGTACAAAAGATTTTAACTTGGATTTGGTATCTGTTTCGAAGAAAGA
Ф	2608 AGTACAAAAGATTTTAACTT	AGTACAAAAGATTTTAACTTGGATTTGGTATCTGTTTCGAAGAAAGA
δ	361 CCACGCATTACAAGTATTTCC	CCACGCATTACAAGTATTTCGCTATGTACACCCGGTTGTAAAAACAGGAGCTCTGATGGGT 420
90	2668 CCACGCATTACAAGTATTTCC	CCACGCATTACAAGTATTTCGCTATGTACACCCGGTTGTAAAACAGGAGCTCTGATGGGT 2727
· VQ	421 TGTAACATGAAAACAGCAAC	TGTAACATGAAAACAGCAACTTGTCATTGTAGTATTCACGTAAGCAAATAA 471
Ф	2728 TGTAACATGAAAACAGCAAC	TGTAACATGAAAAACAGCAACTTGTAATTGTAGTATTCACGTAAGCAAATAA 2778

Searth completed: January 12, 2004, 12:57:03 Job time: 3040 Becs

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Result
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Run on:
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Maximum DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Title:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                               410.4
410.4
358.4
                                                                                                                                                                                                          Score
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seq length: 2000000000
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Gapop 10.0 , Gapext 1.0
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                                                                                                                                                                                                       Match
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767
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                                                                                                                                                                                                                                                                                                                                                                                             /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1989.DAT:
/SIDS1/gcgdata/geneseq/geneseqn-embl/NA1990.DAT:
/SIDS1/gcgdata/geneseq/geneseqn-embl/NA1991.DAT:
/SIDS1/gcgdata/geneseq/geneseqn-embl/NA1991.DAT:
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/SIDS1/gcgdata/geneseq/geneseqn-embl/NA1993.DAT:
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/SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:
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/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:*
/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT:*
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Copyright (c) 1993 - 2004 Compugen Ltd
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SIDS1/gcgdata/geneseq/geneseqn-embl/NA1986.DAT:*
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                                                                                                                                                                                                     Length
                               7454
7423
518
448
1446
1446
                                                                                                                                                                                                          В
                                                                                                                                                                                                       IJ
      AAT29660
AAX87792
AAQ03354
AAQ50288
AAT29611
ABK14453
AAQ30070
AAX87793
                                                                                                                                                                                                                                                                       SUMMARIES
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Nisin nisABTCIP ge
Nisin gene region
Nucleotide fragmen
nisA gene and flan
Nisin A promoter f
Lactococcus lactis
Sequence of the ni
Nisin Z gene of La
                                                                                                                                                                                                   Description
      RESULT 1
AA729660
ID AA727
XX AA72
AC AA72
XX Nisi
DE Nisi
XX Nisi
XX Nisi
XX Lact
XX Lact
XX FT repe
FT repe
FT -35
FT -35
FT RBS
FT CDS
                                                                                                                                                                                                                                                                                                                                                                                                                      Nisin A; nisA gene; antimicrobial; preservative; antibiotic; lantibiotic; protein engineering; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nisin nisABTCIP gene cluster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-AUG-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAT29660;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAT29660 standard; DNA; 7454 BP.
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Tumour suppressor	AAS46803	22	7403	6.1	46.6	45
Human immune syste	ABL32986	24	17294	6.1	46.8	44
Haematopoietic cel	ABZ10246	25	8056	6.1	46.8	43
Human immune syste	ABL32871	24	5303	6.1	46.8	42
Human immune syste	ABL33149	24	5452	•	47	41
Human immune syste	ABL32029	24	7351	6.2	47.2	40
	ABL34026	24	17594	•	48	39
trans	ABK31320	24	11907	6.3	48	38
Signal transductio	ABK31356	24	6065		48	3.7
Human gene regulat	AAS61260	24	6065	6.3	48	36
Chemically treated	ABL70579	24	6065	•	48	35
2	ABQ67094	24	83391		48.2	34
Anopheles gambiae	ABQ75107	24	4985	٠	48.2	ü
Human metastasis a	ABL34557	24	13125		48.4	32
Human immune syste	ABL33227	24	13125		48.4	31
Chemically treated	ABL70284	24	13125		48.4	30
m	AAA70250	21	7143		48.6	29
Human immune syste	ABL33140	24	6361	•	48.8	28
Nucleotide fragmen	AAQ03353	11	830		50.4	27
Haematopoietic cel	ABZ10100	25	8056		51.4	26
AmEPV genome fragm		24	50000		52.2	25
Insertion sequence		14	100	6.9	52.8	24
Human immune syste	ABL33748	24	11805	•	53.4	23
Haematopoietic cel	ABZ10246	25	8056	7.1	54.6	22
•	×	15	1833	<u>.</u>	56.8	21
Genomic sequence		24	2365589	<u>,</u>	58.4	20
		24	3011208	0.1	77.8	19
a innocua	ABQ67197	24	1163020	0.1	77.8	18
innocua	ABQ67737	24	960	÷	77.8	17
		24	930	0.1	77.8	16
		24	878	0.4	80	15
DNA encoding subti		18	144	0.7	81.8	14
Lactose operon pro	AAQ50289	14	546	1.1	84.8	13
1910E	AA169229	24	212	26.4	2	12
bacte	S.	14	321	1.6	319.4	11
LL-2	47	14	321	1.6	319.4	10
Bacteriocin gene.	AAQ49150	14	321	1.6	319.4	ø

0 0 0

## ALIGNMENTS

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-10_signal
                                                                             -35_signal
                                                                                                             repeat_unit
                                                                                                                                            repeat_unit
                                                                                                                                                                             Lactococcus lactis strain NIZO R5.
                                      /label= p1-35
152..157
/*tag=
         /*tag= d
/label= p1-10
191..197
/*tag= e
/*tag= 6
206..379
                                                                                                                                                       Location/Qualifiers
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|08..118
                                                                                                                                  *tag=
                                                                                                    *tag=
                                                                                            type= INVERTED
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The gene cluster nisABTCIPRK (see AAT29660 and AAT29661) of Lactococcus lactis includes the nisA gene coding for pre-nisin A (AAR95267, see also AAR95263) and the genes for nisin modification, secretion and immunity. nisB (AAR95268) and nisC (AAR95270) are believed to be involved in reactions that modify pre-nisin; nisT (AAR95269) is similar to a transport ATPase and is involved in translocation of nisin out of the cell; nisI (AAR95271) is involved in immunity to nisin. Replacement of the natural, chromosomal copy of the nisA gene with a variant nisA gene allows prodn. of high levels of nisin A variants in Lactococcus lactis hosts.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SdO
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                                                                                                                                                                                                                                                                                   Disclosure; Fig 7; 69pp; English.
                                                                                                                                                                                                                                                                                                                                                Making cell which expresses nisin but gene - by providing cell with variant
                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1996-268616/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19-NOV-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20-NOV-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-MAY-1996.
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                                                                                                                                                                                                                                                                                                                              modification, secretion and immunity
                                                                                                                                                                                                                                                                                                                                                                                                                  P-PSDB; AAR95267, AAR95268, AAR95269,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dodd HM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (BIOT-)
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//tabel= nisB
3462..3470
/*tag= m
3479..5281
/*tag= nisT
7/tabel= nisT
7/tag= p
//tabel= nisC
6499..6508
/*tag= p
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6499..6508
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487..3468
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                                                                                                                                                                                                                                                                                                                                                does not contain natural nish nish gene, and genes for nisin
                                                                                                                                                                                                                                                                                                                                                                                                                AAR95270, AAR95271.
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Sequence

7454

2741 A;

920

Ç

1376 G;

2417

T; 0 other;

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RESULT 2
AAX87792
ID AAX8
AXX PARA
AC AAX8
XX O9-N
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XX Nisi
XX Nisi
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XX Feed
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Best Local S
Matches 675
                                                                                                                                                                                      Nisin A; nis
nisin I; nis
                                                                                                                                                                                                                                                                Nisin gene region of Lactobacillus lactis.
                                                                                                                                                                                                                                                                                                                  09-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                  AAX87792;
                                                                                                                                                                                                                                                                                                                                                                                                              AAX87792 standard; DNA; 7423
                                                                                                                     Lactobacillus lactis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TATTCACGTAAGCAAATAACCAAATCAAAGGATAGTATTTTGTTAGTTCAGACATGGATA
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                                                                                                                                                               A; nisin B; nis B; nisin T; nis T; nisin C; nis I; lantibiotic; animal performance; growth rate ion; bacteriocin; probiotic; ss.
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                                               Location/Qualifiers
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                                                                                              This is the nisin gene region of Lactobacillus lactis NIZO R5, including the nis A, nis B, nis T, nic C and nis I genes that respectively code for nisins A, B, T, C and I (see AAY06665-69). The invention relates to methods of enhancing performance in an animal by administering a bacterium capable of expressing a performance enhancing polypeptide such as nisin A or nisin Z. The enhanced performance results in improved growth rates and feed conversion efficiencies. The bacterium, which may be genetically modified to express the performance enhancing polypeptide, is sufficient to express the performance enhancing polypeptide, is a embryo or neonatal animal. If the polypeptide is nisin, it may also inhibit ruminal methane, decrease acetate to propionate ratios and prevent amino acid deamination. Administration of an appropriate bacterium which may act as a probiotic may also help control enteric pathogens in poultry. The polypeptide is produced continuously in the gut, maintaining a constant level. The protein is eventually degraded, leaving no residues in the meat.
                                          Query Match
Best Local Similarity
Matches 643; Conserv
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                                                                                 Sequence
                                                                                                                                                                                                                                                                     Disclosure; Page 55-57; 79pp; English.
                                                                                                                                                                                                                                                                                       Novel performance enhancing method resulting in improved growth rates and feed conversion efficiencies in animals
                                                                                                                                                                                                                                                                                                                  P-PSDB; AAY06665, AAY06666, AAY06667, AAY06668, AAY06669
                                                                                                                                                                                                                                                                                                                                              Flanagan AJ,
                                                                                                                                                                                                                                                                                                                                                                                            18-FEB-1998;
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                                                                                                                                                                                                                                                                                                                                                               (PFIZ ) PFIZER INC. (PFIZ ) PFIZER LTD.
                                                                                                                                                                                                                                                                                                                             1999-527402/44.
                         125 GAAACATTAACAAATCTAAAACAGTCTTAATTCTATCTTGAGAAAGTATTGGTAATAATA 184
                                                                                 7423
       Conservative
                                                                                 BP; 2729 A; 913 C; 1374 G; 2407 T; 0 other;
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                                            Score 643; DB 20; 1; Pred. No. 3.8e-120; 0; Mismatches 0;
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Nisin precursor peptide; peptide leader fragment; peptide leader sequence; post-translational modification; Streptococcus lactis ATCC 11454.
                                                                                                                                                                                                                                                                                                                              Streptococcus lactis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleotide fragment containing gene encoding nisin peptide derived from Stretococcus lactis ATCC 11454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAQ03354 standard; DNA; 518
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 518;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                It contains a gene leader fragment encoding peptide leader sequence which induce post-translational modification (PTM) of amino acids Cys, Ser and Thr. The nisin gene was found in S. lactis using 20mer probe (see FT tag f). A DNA fragment is prepared encoding a precursor polypeptide attached to a leader fragment, this is then inserted into an expression vehicle to express and modify the precursor polypeptide. Modified proteins containing debydroalanine and debydrobutyrine which can covalently bind to targets, and adhesives for specific substrates can be designed. Tag b is claimed in the patent in claim 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 518 BP; 187 A; 74 C; 89 G; 168 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1990-051685/07.
P-PSDB; AAR05238.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Fig 3; 19pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Leader peptide sequence -
including post-translational modification of polypeptide(s)
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AGGATAGTATTTTGTTAGTTCAGACATGGATACTATCC 518
                                                               TGTAACATGAAAACAGCAACTTGTCATTGTAGTATTCACGTAAGCAAATAACCAAATCAA 480
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                                              TGTAACATGAAAACAGCAACTTGTCATTGTAGTATTCACGTAAGCAAATAACCAAATCAA
                                                                                                        CCACGCATTACAAGTATTTCGCTATGTACACCCGGTTGTAAAAACAGGAGCTCTGATGGGT
                                                                                                                          CCACGCATTACAAGTATTTCGCTATGTACACCCGGTTGTAAAACAGGAGCTCTGATGGGT
                                                                                                                                                                                                                                                                                                             AATATTATTGTCGATAACGCGAGCATAATAAACGGCTCTGATTAAATTCTGAAGTTTGTT
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                                                                                                                                                                                                                                                                                                                                                                                                  GAGATAGGTTTATTGAGTCTTAGACATACTTGAATGACCTAGTCTTATAACTATACTGAC
                                                                                                                                                              AGATACAATGATTTCGTTCGAAGGAACTACAAAATAAATTATAAGGAGGCACTCAAAATG
                                                                                                                                                                                                                                                   AGATACAATGATTTCGTTCGAAGGAACTACAAAATAAATTATAAGGAGGCACTCAAAATG
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/note="20mer probe"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 518; DB 11;
Pred. No. 3.9e-95;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 11; Length 518;
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RESULT 4
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                                                                     bacteria e.g. strains of lactococcus lactis. It has efficient antimicrobial activity against a wide range of Gram positive bacteria which are food pathogens or spoilage organisms. The genes involved in nisin maturation can be used to transform other microbes which are unable to secrete the natural nish nisin. These organisms can however modify nisin and translocate it out of the cell. This provides an effective means of producing variant nisins which are useful as antimicrobial agents in conditions of high pH where natural nisin is ring-opened and lose its antimicrobial properties.
Sequence 448
                                                                                                                                                                                                                                                                                                                                                                                                                                New organisms able to express genes for nisin maturation, native pre-nisin - useful for producing variant nisin(s) antimicrobial use in food industry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1993-336920/42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-APR-1993;
                                                                                                                                                                                                                                                                                                Nisin is a highly modified peptide antibiotic produced by certain bacteria e.g. strains of Lactococcus lactis. It has efficient
                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Figure 2; 62pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nisin; antibiotic; food; spoilage; pathogens; industrial processes; lantibiotic; Lactococcus lactis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nisA gene
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03-MAY-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lactococcus lactis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (AGRI-)
                                                       (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      481 AGGATAGTATTTGTTAGTTCAGACATGGATACTATCC 518
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BP;
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(first entry)
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/label= nisB gene
/note= "continues
167 A; 64 C;
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/note= "Inverted repeat."
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label= nisA
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not given in
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  80 G; 137 T; 0 other;
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Query Match Best Local Similarity Matches 448; Conserv

58.4%; Score 448; DB 14; ilarity 100.0%; Pred. No. 4.4e-81; Conservative 0; Mismatches 0;

DB 14; Length 448; 4.4e-81; es 0; Indels

0

Gaps

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ARESULT 5
AAT2961
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ID AAT2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nisin Z; lactococcus; lactic acid bacterium; promoter; membrane protein; antimicrobial peptide; nisin A; cell lysis; enzyme; fermented foodstuff; extracellular protein; dairy product; cheese; yoghurt; inducer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAT29611 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nisin A promoter fragment.
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                                                 De Vos WM,
                                                                                                                                                 18-NOV-1994;
18-NOV-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lactococcus lactis.
WPI; 1996-252838/26
                                                                                                                                                                                                                            17-NOV-1995;
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                                                                                                  (NIZO-) NIZO STICHTING NEDERLANDS
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                                                 Kuipers OP
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94NL-0001934.
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1278..1283
/*tag= b
1332..1446
/*tag= c
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1252..1257
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Controlled lysis of transformed lactic acid bacteria to release intracellular proteins or RNA - by addn. of inducer to activate promoter to express antimicrobial peptide, useful for prodn. of
                                                                                                                                                    dairy prods.
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Example 2; Fig 4b; 29pp; English

This sequence represents the nisin A promoter isolated from Lactococcus CC lactis. This sequence is used to control the DNA fragment of the method CC of the invention. The method of the invention is for the controlled CC expression of a DNA fragment containing one or more genes of desired CC characteristics, in a lactic acid bacterium. The DNA fragment is under CC the control of a promoter for a microbial gene that encodes an CC expressed by the addition of a suitable inducer for transcription CC expressed by the addition of a suitable inducer for transcription CC expression of the DNA fragment causes the lysis of the microorganism CC used is an antimicrobial peptide produced by lactic acid bacterium. The CC expression of the DNA fragment causes the lysis of the microorganism CC used, or alternatively results in the release of intracellular proteins CC (such as enzymes, membrane proteins, extracellular proteins and CC used, or alternatively results in the release of intracellular proteins of rothe microorganism CC used, or alternatively results in the release of intracellular proteins of continuity of products containing a desired protein. The release of CC into the medium. The method can be used for the production of proteins of CC intracellular enzymes provides accelerated maturing of fermented CC the intracellular enzymes provides accelerated maturing of fermented CC into the can be used to determine the concentration of a inducer in CC addition of the inducer.

Sequence 1446 BP; 488 A; 233 C; 244 G; 481 T; 0 other;

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Best Local :
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1395
                            361
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                                                                                                                                                                                                                                                                                                                                  61
                                                                                                                                                                                                                                                                                                                                                                                  1 AGTTGACGAATATTTAATAATTTTAATTAATATCTTGATTTTCTAGTTCCTGAATAATATA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                          h 53.5%;
Similarity 99.8%;
                                                                                                                                                                                                                                                            AATAGAAACATTAACAAATCTAAAACAGTCTTAATTCTATCTTGAGAAAGTATTGGTAAT 180
                                                                                                                                                                                                                                                                                                    GAGATAGGTTTATTGAGTCTTAGACATACTTGAATGACCTAGTCTTATAACTATACTGAC
                                                                                                                                                                                                                                                                                                                       GAGATAGGTTTATTGAGTCTTAGACATACTTGAATGACCTAGTCTTATAACTATACTGAC 120
                                                                                                                                                                                                                                                                                                                                                                AGTTGACGAATATTTAATAATTTAATATATCTTGATTTTCTAGTTCCTGAATAATATA
CCACGCATTACAAGTATTTCGCTATGTACACCCCGTTGTAAAACAGGAGCTC
                 CCACGCATTACAAGTATTTCGCTATGTACACCCGGTTGTAAAACAGGAGCTC
                                                                              AGATACAATGATTTCGTTCGAAGGAACTACAAAATAAATTATAAGGAGGCACTCAAAATG
                                                                                                                                    AGATACAATGATTTCGTTCGAAGGAACTACAAAATAAATTATAAGGAGGCACTCAAAATG
                                                                                                                                                                                AATATTATTGTCGATAACGCGAGCATAATAAACGGCTCTGATTAAATTCTGAAGTTTGTT
                                                                                                                                                                                                            AATATTATTGTCGATAACGCGAGCATAATAAACGGCTCTGATTAAATTCTGAAGTTTGTT 240
                                                                                                                                                                                                                                          AATAGAAACATTAACAAATCTAAAACAGTCTTAATTCTATCTTGAGAAAGTATTGGTAAT 1214
                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 410.4; DB 17; Length 1446; Pred. No. 1.7e-73;
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 1446
                               412
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RESULT 6
ABK14453
ID ABK1
XX
AC ABK1
XX
AC ABK1
XX
AC ABK1
XX
XX

ABK14453 standard; DNA; 1446

ВP

08-MAY-2002 ABK14453;

(first entry)

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The present invention relates to a new method for controlling expression CC of a gene. The method of the invention involves providing a DNA fragment CC comprising a gene under transcriptional control of a promoter, where the CC promoter is obtained from a Gram-positive gene for an antimicrobial control of a precursor of the peptide. The gene is found in a gene CC cluster for the synthesis of the antimicrobial peptide and the promoter is inducible by the peptide. The antimicrobial peptide of the invention CC is acceptable in food products. The method provides a homologous CC expression system in Lactococcus, which is able to give strict/absolute cregulation of the gene expression using (in low concentrations) suitable inducers. High production of the desired protein, aminopeptidase N in experiments, gave a specific activity of 25000 nmol/mg/min using 0.5 g/l clisin A as the inducer, a level that has never been reached before by use of other (constitutive) promoters. The present nucleic acid sequence correspondents the nish promoter sequence of the invention.
                                                                                                                                                                                                                                                                       Matches
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Controlled expression of a gene for production of a protein comprises providing a DNA fragment under control of a promoter from an antimicrobial peptide, where the peptide induces the promoter
                                                                                                                                                                                                                                                                                                                                                           Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kuipers
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18-NOV-1994;
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                                                                                                                                   61
                                                                                                                                                                                                                                                                       411;
                                                                                                                                                                                                                                                                                            Similarity
                                                                                                            GAGATAGGTTTATTGAGTCTTAGACATACTTGAATGACCTAGTCTTATAACTATACTGAC
                    AATAGAAACATTAACAAATCTAAAACAGTCTTAATTCTATCTTGAGAAAGTATTGGTAAT
                                                                                     GAGATAGGTTTATTGAGTCTTAGACATACTTGAATGACCTAGTCTTATAACTATACTGAC
AATAGAAACATTAACAAATCTAAAACAGTCTTAATTCTATCTTGAGAAAGTATTGGTAAT
                                                                                                                                                                             AGTTGACGAATATTTAATAATTTTAATAATATCTTGATTTTCTAGTTCCTGAATAATATA
                                                                                                                                                                                                           AGTTGACGAATATTTAATAATTTTAATATATCTTGATTTTCTAGTTCCTGAATAATATA
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                                                                                                                                                                                                                                                                     Conservative
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94NL-0001935.
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/standard_name= "
1317..1323
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1252..1257
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/standard_name=
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1278..1283
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                                                                                                                                                                                                                                                                                     53.5%;
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                                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                                                   Score 410.4;
Pred. No. 1.7e
0; Mismatches
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.1.7e-73;
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                                                                                                                                                                                                                                                                                                               1446;
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                                                                                                                                                                                                                                                                   Gaps
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밁 S 밁 Ś 밁 S

Total DNA was isolated from the L. lactis strains NIZO 22186 and NIZO R5. With the aid of the nisA gene of strain NIZO R5 as a p. a 4.5 kb HindIII fragment was identified in the total DNA strain NIZO 22186, which was then cloned in M13 mpl8. The DNA sequence

sequence of a probe,

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RESULT 7
AAQ30070
ID AAQ30070

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                                                                                                             Example; Fig
                                                                                                                                                                          New lantiobiotic cpds. relations, which produce them,
                                                                                                                                                                                                                                                                              WPI;
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02-APR-1993
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                                                                                                                                                                                                                                                                                                                                                                     OZIN (-OZIN)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nisin Z; nisin A; analogue; food preservative; ss
                                                                                                               3; 42pp;
                                                                                                                                                                                                                                                                                                                                                                   STICHTING NEDERLANDS INST ZUIVELOND
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21..40
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/label= primer
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                                                                                                               English.
                                                                                                                                                                                 related to nisin A - and Lactococcus chem, useful as preservatives for foods
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Best Local Similarity 99.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the gene for nisin Z production (nisZ) was determined by making use of oligos complementary to the 5 and 3 flanking sequences of the nisA gene. The nucleotide sequence of the nisZ gene is found to be identical to that of the nisA gene with the exception of a C to A transversion in posn. 148 which results in the replacement of AA HisZ7 by AsnZ7. The above indicate that the structure of nisin Z is as shown in AARZ8299.
              Flanagan AJ,
                                                                                                                                         26-AUG-1999.
                                                                                                                                                                                                                                                                                                               Nisin
                                                                                                                                                                                                                                                                                                                                         Nisin Z gene of Lactobacillus lactis.
                                                                                                                                                                                                                                                                                                                                                                       09-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                            AAX87793 standard; DNA; 360 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 360 BP; 129 A; 52 C; 66 G;
                                                                                   18-FEB-1998;
                                                                                                             12-FEB-1999;
                                                                                                                                                                     WO9941978-A1
                                                                                                                                                                                                                                                                     Lactobacillus lactis.
                                          (PFIZ ) PFIZER INC. (PFIZ ) PFIZER LTD.
                                                                                                                                                                                                                                                                                            n Z; nis Z; lantibiotic; animal performersion; bacteriocin; probiotic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   301
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             Haxell
                                                                                   98GB-0003424
                                                                                                               99WO-IB00250
                                                                                                                                                                                                          /*tag=
                                                                                                                                                                                                                                         Location/Qualifiers
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              Rolph
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                                                                                                                                                                                                                                                                                                           animal performance; growth
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                TP
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AAQ49150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CC strain 22186. Nisin Z (nis Z) gene region of Lactobacillus lactis companies to methods of a lanthionine-containing bacteriocin. The invention containing the containing bacteriocin. The invention containing the containing bacteriocin. The invention containing bacteriocin. The invention containing performance. The invention containing performance in an animal by administering a bacterium capable of expressing a performance containing polypeptide such as nisin A or nisin Z. The enhanced contained to the generically modified to efficiencies. The bacterium, which may be genetically modified to express the performance enhancing polypeptide, is administered to the gastrointestinal tract, especially to an embryo or meonatal continual. If the polypeptide is nisin, it may also inhibit ruminal methane, decrease acetate to propionate ratios and prevent amino caid deamination. Administration of an appropriate bacterium which may act as a probiotic may also had continuously in the gut, maintaining a constant level. The protein is eventually degraded, it leaving no residues in the meat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                  Bacteriocin
                                                                                                                                                     AAQ49150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel performance enhancing method resulting in improved growth rates and feed conversion efficiencies in animals
              Lactococcus lactis
                                                       Bacteriocin;
                                                                                                            25-MAR-2003
10-MAR-1994
                                                                                                                                                                                 AAQ49150 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 360 BP; 129 A; 52 C; 66 G; 113 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 71; 79pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1999-527402/44.
                                       eriocin; LL-2; gram positive bacteria; antimicrobial; food;
polymerase chain reaction; amplification; inhibit; ss.
                                                                                                                                                                                                                                                       301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAAAGGATAGTATTTTGTTAGTTCAGACATGGATACTATCCTATTTTTATAAGTTATTTA 537
                                                                                                                                                                                                                                                                                                                            GGTTGTAACATGAAAACAGCAACTTGTCATTGTAGTATTCACGTAAGCAAATAACCAAAT 477
                                                                                                                                                                                                                                                                                                                                                                                   TCACCACGCATTACAAGTATTTCGCTATGTACACCCGGTTGTAAAACAGGAGCTCTGATG
                                                                                                                                                                                                                                                                                                                                                                                                                            AATAATATTATTGTCGATAACGCGAGCATAATAAACGGCTCTGATTAAATTCTGAAGTTT
                                                                                                                                                                                                                                                                                                            GGTTGTAACATGAAAACAGCAACTTGTAATTGTAGTATTCACGTAAGCAAATAACCAAAT
                                                                                                                                                                                                                                                                                                                                                                     TCACCACGCATTACAAGTATTTCGCTATGTACACCCGGTTGTAAAACAGGAGCTCTGATG
                                                                                  gene.
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                                                                                                            (updated)
(first en
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Pred. No. 4.3e-63;
0; Mismatches 1
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Best Local Similarity
Matches 320; Conserv
                                                                                                                                                                                                                                                                                                                                                                        The sequence (AAQ49150) was amplified using primers (AAQ49151-52). encoded protein inhibits selected gram positive bacteria and this property is enhanced if further purified by HPLC. The materials being treated to provide inhibition are preferably foods, although other materials can be treated. (Updated on 25-MAR-2003 to correct PF field.)
25-MAR-2003
12-MAY-1993
                            AAQ34782;
                                             AAQ34782 standard;
                                                                                                                                                                                                                                                                                                                                                       Sequence 321 BP; 114 A; 51 C; 63 G; 93 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 13-14 (col 15,16,17,18); 14pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteriocin from Lactococcus lactis subspecies lactis inhibitory against Gram-positive bacteria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUL-1991;
14-MAY-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cbs
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                                                                                                                                                                                                                                                                                           CGCGAGCATAATAAACGGCTCTGATTAAATTCTGAAGTTTTGTTAGATACAATGATTTCGT
                                                                                                      GTTCAGACATGGATACTATCC 518
                                                                                                                                         AACTIGTCATIGTAGTATTCACGTAAGCAAATAACCAAATCAAAGGATAGTATTTIGTTA
                                                                                                                                                                                                                 CTTGGATTTGGTATCTGTTTCGAAGAAAGATTCAGGTGCATCACCACGCATTACAAGTAT
                                                                                                                                                                                                                                                      TCGAAGGAACTACAAAATAAATTATAAGGAGGCACTCAAAATGAGTACAAAAGATTTTAA
                                                                                                                                                                             TTCGCTATGTACACCCCGGTTGTAAAACAGGAGCTCTGATGGGTTGTAACATGAAAAACAGC
                                                                                                                                                                                                       CTTGGATTTGGTATCTGTTTCGAAGAAAGATTCAGGTGCATCACCACGCATTACAAGTAT
                                                                                                                                                                                                                                           TCGAAGGAACTACAAAATTATAAGGAGGCACTCAAAATGAGTACAAAAGATTTTAA
                                                                                                                                                                                                                                                                                CGCGAGCATAATAAACGGCTCTGATTAAATTCTGAAGTTTGTTAGATACAATGATTTCGT
                                                                                          GTTCAGACATGGATACTATCC 321
                                                                                                                               AACTTGTAATTGTAGTATTCACGTAAGCAAATAACCAAATCAAAGGATAGTATTTTGTTA
                                                                                                                                                                   TTCGCTATGTACACCCGGTTGTAAAACAGGAGCTCTGATGGGTTGTAACATGAAAACAGC
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                                                                                                                                                                                                                                                                                                                   41.6%;
ilarity 99.7%;
Conservative
(updated)
(first entry)
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92US-0882079.
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/product= Bacteriocin
                                             DNA;
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                                                                                                                                                                                                                                                                                                                   Score 319.4; DB 14; Length 321; Pred. No. 2.9e-55; o; Mismatches 1; Indels. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  English.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUL-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUL-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sig_peptide
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                                 GTTCAGACATGGATACTATCC 518
                   GTTCAGACATGGATACTATCC 321
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101..169
/*tag= b
170..271
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                                                                                                                                                                                                                                                   41.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene
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Lactococcus lactis sub-species lactis
  NRRL B-18809
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INT FLAVORS & FOOD INGREDIENTS

Marugg JD, Vanwassenaar g

Inhibition of Gram-positive bacteria - using bacteriocin from Lactococcus lactis sub-species lactis NRRL B-18809 derived

The sequence is that of the bacteriocin LL-2 precursor gene, the precursor can be used in a method for the inhibition of Gram-positive bacteria. LL-2 is especially useful for treatment of food, although other non-food materials may also be treated.

(Updated on 25-MAR-2003 to correct PA field.)

Sequence 321 BP; 114 A; 51 C; 63 G; 93 T; 0 other;

Score 319.4; DB 1 Pred. No. 2.9e-55; Mismatches DB 14; 1: Indels Length 321; 0 Gaps 0

TCGAAGGAACTACAAAATAAATTATAAGGAGGCACTCAAAATGAGTACAAAAGATTTTAA CGCGAGCATAATAAACGGCTCTGATTAAATTCTGAAGTTTGTTAGATACAATGATTTCGT CGCGAGCATAATAAACGGCTCTGATTAAATTCTGAAGTTTGTTAGATACAATGATTTCGT TCGAAGGAACTACAAAATAAATTATAAGGAGGCACTCAAAATGAGTACAAAAGATTTTAA 120 317 60 257

CTTGGATTTGGTATCTGTTTCGAAGAAAGATTCAGGTGCATCACCACGCATTACAAGTAT CTTGGATTTGGTATCTGTTTCGAAGAAAGATTCAGGTGCATCACCACGCATTACAAGTAT 377 180

AACTIGTCATTGTAGTATTCACGTAAGCAAATAACCAAATCAAAGGATAGTATTTTGTTA TTCGCTATGTACACCCGGTTGTAAAACAGGAGCTCTGATGGGTTGTAACATGAAAACAGC TTCGCTATGTACACCCGGTTGTAAAACAGGAGCTCTGATGGGTTGTAACATGAAAACAGC 497 437 300 240

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                                                                                                                                                                                                                          Best Local Similarity Matches 320; Conserv
                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                     The isolated bactriocin obtained from the polypeptide precursor has an inhibitory activity against selected Gram positive bacteria. The amount of bacteriocin required to provide inhibition is 15-100 arbitrary units per gram of material. The materials being treated with the bacteriocin to provide inhibition are especially foodstuffs
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Isolated and purified polypeptide from Lactococcus lactis sub species lactis - has inhibitory activity against gram-positive bacteria for e.g. food etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Henderson JT,
                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Column 17-18; 13pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUL-1991;
14-MAY-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-MAR-2003
21-JAN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAQ46818;
                                                                                                                                                                                                                                                                                 Sequence 321 BP; 114 A; 51 C; 63 G; 93 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (UNIL ) QUEST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14-MAY-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAQ46818 standard; DNA;
                                                                                                                                                                                                                                                                                                        with the bactericcin to provide inhibition are especially (Updated on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lactococcus lactis (subspecies lactis)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1993-249768/31.
DB; AAR39312.
 181
                                                       121
                                                                                  318
                                                                                                                                        258
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                                                                                                                                                                    .
                                                                                                                              TCGAAGGAACTACAAAATAAATTATAAGGAGGCACTCAAAATGAGTACAAAAGATTTTAA 317
                                                                                                                                                                                    CGCGAGCATAATAAACGGCTCTGATTAAATTCTGAAGTTTTGTTAGATACAATGATTTCGT
                    TTCGCTATGTACACCCGGTTGTAAAACAGGAGCTCTGATGGGTTGTAACATGAAAACAGC
TTCGCTATGTACACCCGGTTGTAAAACAGGAGCTCTGATGGGTTGTAACATGAAAAACAGC
                                                      CTTGGATTTGGTATCTGTTTCGAAGAAAGATTCAGGTGCATCACCACGCATTACAAGTAT
                                                                                  CTTGGATTTGGTATCTGTTTCGAAGAAAGATTCAGGTGCATCACCACGCATTACAAGTAT 377
                                                                                                            TCGAAGGAACTACAAAATAAATTATAAGGAGGCACTCAAAATGAGTACAAAAGATTTTAA
                                                                                                                                                                    CGCGAGCATAATAAACGGCTCTGATTAAATTCTGAAGTTTGTTAGATACAATGATTTCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                bacteriocin coding sequence
                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      inhibition; polypeptide; Lactococcus lactis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (updated)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INT FLAVORS & FOOD INGREDIENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Marugg JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               91US-0721774.
92US-0882715.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "The bacteriocin comprises the 34 terminal
amino acids of the polypeptide precursor."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag= a
/product= Bacteriocin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                     41.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Vanwassenaar PD,
                                                                                                                                                                                                                          0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ВÞ
                                                                                                                                                                                                                       Score 319.4; DB 14; Length Pred. No. 2.9e-55; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Vedamuthu ER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8
                                                                                                                                                                                                                                                   Length 321;
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                                                                                                                                                                                                                       Gaps
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240
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This invention describes a novel plasmid (I), designated pCD6 for CC transformation of Clostridium difficile. The invention describes a method CC l) for (a) expressing a heterologous gene sequence in C. difficile which CC comprises providing a plasmid containing the heterologous gene sequence, introducing the plasmid into C. difficile, and optionally, where the CC plasmid also contains a gene coding for a selectable marker, selecting CC for C. difficile that express the selectable marker; (2) for making a CC difficile that express the selectable marker; (2) for making a CC omprises; (3) for identifying a C. difficile virulence factor which CC comprises culturing C. difficile in the absence of, and in the presence of a regulating factor that promotes expression of C. difficile virulence factors and identifying a putative virulence factor whose expression is reduced in the absence of the regulating factor; (4) for identifying a vector that integrates into a gram positive bacterial genome which CC comprises; (a) transforming a gram positive bacteria with a plasmid, where the plasmid includes a sequence of a inducer of the promoter, where the plasmid comprises an inducible promoter and replication of the transforming a gram positive bacteria with a plasmid the containing a gram positive bacteria with a plasmid the containing a gram positive bacteria where the promoter, and selecting for bacteria with a plasmid comprises an suppressible promoter and replication of the plasmid comprises an suppressible promoter and replication of the plasmid comprises an suppressible promoter and replication of the plasmid comprises an suppressible promoter and replication of the plasmid comprises and suppressible promoter and replication of the plasmid comprises and suppressible promoter and replication of the plasmid comprises and suppressible promoter and replication of the plasmid comprises and suppressible promoter and replication of the plasmid comprises and comprises and comprises contained the plasmid comprises contained the 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Plasmid pMTL910E; integration;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAI69229;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (MICR-) MICROBIOLOGICAL RES AUTHORITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -35_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          plasmid, designated pCD6, useful for transformation of Clostridium ficile and for expressing gene in Clostridium difficile
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             498
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Fig 12; 60pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pMTL910E
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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94..100
/*tag= b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers 71..77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Elmore MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            88
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RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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                                                         antimicrobial use in food industry
                                                                                         New organisms able to express genes for nisin maturation, native pre-nisin - useful for producing variant nisin(s)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eschericia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nisin; antibiotic; food; spoilage; pathogens; industrial processes; lantibiotic; Lactococcus lactis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-MAR-2003 (updated)
03-MAY-1994 (first entry)
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                                                                                                                                                                                      WPI; 1993-336920/42.
                                                                                                                                                                                                                                                Dodd HM,
                                                                                                                                                                                                                                                                                                                                                                          02-APR-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                       01-APR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-OCT-1993.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lactose operon promoter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAQ50289 standard; DNA; 546 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            plasmid includes a sequence coding for a selectable marker, and the
                                                                                                                                                                                                                                                                                                             (AGRI-) AGRIC & FOOD RES COUNCIL.
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                                                                                                                                                                                                                                                Gasson MJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAATAAATTATAAGGAGGCACTCGACAATATT 212
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97.2%;
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Disclosure; Figure 5; 62pp; English

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AAXABOTIT 14
AAXABOTIT 14
AAXABOTIT 10
AAXABOTIT 11
AC AAXABOTIT 10
AC Chime
COS COTIT
AC AAXABOTIT
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Matches 86;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-NOV-1999
Lantibiotic mutants and chimera(s) - activity compared to nisin
                                                                              WPI; 1997-225847/20.
P-PSDB; AAY31659.
                                                                                                                                                                                                                                                                  28-SEP-1995;
                                                                                                                                                                                                                                                                                                                      30-SEP-1996;
                                                                                                                                                                                                                                                                                                                                                                          03-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                             WO9711713-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chimeric -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        preservative;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nisin; subtilin; lantibiotic; chimera; mutant; bacteriocide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA encoding subtilin-nisin chimera.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAX87829;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAX87829 standard; DNA; 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 546 BP; 229 A; 62 C; 78 G; 177 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chimeric
                                                                                                                                                                                                              (UYMA-) UNIV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               h 11.1%;
Similarity 97.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AATAAATTATAAGGAGGCACTCAAAATG 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lactococcus lactis. Bacillus subtilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                              MARYLAND BALTIMORE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "Sub(1-11)-Nis(12-32)'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "subtilin signal peptide"
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Pred. No. 4.1e-08;
                           having
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                             stability
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Example; Fig 2; 60pp; English.

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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       provides lantibiotic mutants and chimeras (see also AAY31658) ha enhanced activity and stability compared to nisin and subtilin. The year be produced by cultivation of transformed host cells an used e.g. as food preservatives to treat, kill or inhibit the growth of microorganisms and/or their spores.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY31659) composed of a subtilin leader region and a subtilin-nisin fusion comprising residues 1-11 of Bacillus subtilis subtilin and residues 12-12 of Lactococcus lactis nisin. The chimera was not efficiently processed by B. subtilis into a functional lantibiotic. A heterogeneous mixture of products was produced, none of the products having the expected properties of a correctly processed polypertide. However, the mixture contained a minor component with
                                    New genomic sequences from Listeria species, useful treatment and prevention of infection, also related antibodies and modulators -
                                                                                                                         Kunst F,
                                                                                                                                                     (INSP )
                                                                                                                                                                                             04-OCT-2000; 2000FR-0012697
                                                                                                                                                                                                                         04-OCT-2001; 2001WO-FR03061.
                                                                                                                                                                                                                                                                               WO200228891-A2
                                                                                                                                                                                                                                                                                                       Listeria monocytogenes 4b
                                                                                                                                                                                                                                                                                                                                    Antibacterial; Listeria; food contamination; mutational analysis; infection; ds.
                                                                                                                                                                                                                                                                                                                                                                             Listeria monocytogenes 4b contig DNA sequence #128.
                                                                                                                                                                                                                                                                                                                                                                                                          29-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                     ABQ70186;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABQ70186 standard; DNA; 878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 144 BP; 49 A; 32 C; 32 G; 31 T; 0 other;
                                                                                              WPI; 2002-332479/37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This polynucleic acid (I) encodes
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                                                                                                                                                   INST PASTEUR.
CNRS CENT NAT RECH SCI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GATTCAGGTGCATCACGCATTACAAGTATTTCGCTATGTACACCCCGGTTGTAAAACA 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAATAACCAAATCAAAGGATA 486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GATTCGAAAATCACTCCGCAATGGAAAAGTGAATCACCTTGTACACCCGGGTGTAAAAACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAATAGGTAACCAAATAGGTA 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGCGCCCTGATGGGTTGTAACATGAAAACAGCCACGTGTCATTGTAGTATTCACGTAAGC
                                                                                                                      Glaser P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ВÞ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 81.8;
Pred. No. 1.
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                                                  for detection, polypeptides,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    <u>,</u>
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Claim 14; SEQ ID 2999; 180pp; French

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                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to nucleic acid sequences (ABQ67188-ABQ71212) from Listeria sp. The sequences are useful as probes and primers for identification and/or detection of Listeria (e.g. as contaminants in foods, or mutational analysis) and for analysis of gene expression. Proteins encoded by the nucleic acid sequences can be used to screen for compounds that modulate gene expression, replication and pathogenicity of Listeria (potential therapeutic agents), also for
                                                                                                                                                                                                                                                                                                                                                                                                      anti-Listeria vaccines.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic fo directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                             Sequence 878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           treating infections by Listeria,
883
                                                                       628
                                                                                                                                                568
                                 183
                                                                                                          123 TAGAAACATTAACAAATCTAAAACAGTCTTAATTCTATCTTGAGAAAGTATTGGTAATAA
                                                                                                                                                                                                                           508 TTGATAAATGGCGTATAATTCTATCATTATCTTGATTCTCCAATTCCTGAATAATATGAA
                                                                                                                                                                                     63
                                                                                                                                                                                                                                                            3 TTGACGAATATTTAATAATTTTATTAATATCTTGATTTCTAGTTCCTGAATAATATAGA
TAGT 691
                               TATT 186
                                                                     TCGAAACTCCAGCATATAATAGCAAAGATGCATGGGTATGTCATAAACTATGAATCGTAA
                                                                                                                                                GATATGTTTCCTGGGTAGTAGTCATACTTGAATGACCTAACCTATTCGCAACACTAGCAA
                                                                                                                                                                                     GATAGGTTTATTGAGTCTTAGACATACTTGAATGACCTAGTCTTATAACTATACTGACAA
                                                                                                                                                                                                                                                                                                                                                                             BP; 304 A; 132 C; 136 G; 305 T; 1 other;
                                                                                                                                                                                                                                                                                                                     10.4%;
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Pred. No. 3.9e-07;
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                                                                                                                                                                                                                                                                                                    65;
                                                                                                                                                                                                                                                                                                                                       Length 878;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             as immunogens
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Search completed: January 12, Job time: 280 secs 2004, 11:30:05

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Perfect score:
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1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*

2: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*

3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*

5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

5: /cgn2_6/ptodata/1/ina/backfIles1.seq:*
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    GenCore version 5.1.6 (c) 1993 - 2004 Compugen
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US-08-773-731A-1
US-08-560-007B-1
US-08-129-151A-1
US-08-129-151A-1
US-08-129-175-1
US-07-721-774A-1
US-07-882-775-1
US-07-882-775-1
US-08-836-687B-22
US-08-836-687B-22
US-08-836-687B-27
US-08-773-731A-3
US-08-773-731A-7
US-08-781-525-6
US-08-793-731A-7
US-08-793-731A-7
US-08-793-731A-7
US-08-793-731A-7
US-08-793-731A-7
US-08-7981-525-8
US-08-86-617-6
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US-08-86-617-8
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APPLICANT: Dodd, Helen Mair
TITLE OF INVENTION: PRODUCTION OF VARIANT NISIN
FILE REFERENCE: 20747/70
CURRENT APPLICATION NUMBER: US/08/836,687B
CURRENT FILING DATE: 1995-11-20
NUMBER OF SEQ ID NOS: 51
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 29
LENGTH: 7454
TYPE: DNA
ORGANISM: Lactococcus sp.
US-08-836-687B-29
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US-08-836-687B-29
; Sequence 29, Application
; Patent No. 6448034
; GENERAL INFORMATION:
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Similarity 100.0%; Pred. No. 2.2e-140;
75; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                      TATTCACGTAAGCAAATAACCAAATCAAAGGATAGTATTTTGTTAGTTCAGACATGGATA
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US-08-465-4791-1
US-08-986-6.77-1
US-08-773-731A-21
US-08-7981-5.5-3
US-08-220-033-3
US-08-465-491-3
US-08-986-6.17-3
US-08-986-6.17-3
US-08-986-6.17-3
US-08-986-6.35-4
US-08-920-827-6
US-08-920-827-6
US-08-921-177-6
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US-08-921-828-6
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RESULT 2
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                                                                                                   TELEPAX: 202-887-000
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 448 base pairs
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                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ver
RENT APPLICATION NUMBER: US/08/773,731A
FILING DATE: 24-DEC-1996
CLASSIFICATION 1435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/313,123
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB93/00676
FILING DATE: 01-APR-1993
PRIOR APPLICATION NUMBER: GB 9207267.7
APPLICATION NUMBER: GB 9207267.7
FILING DATE: 02-APR-1992
PRIOR APPLICATION NUMBER: GB 9207267.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: DICKSTEIN, SHAPIRO, MORIN & OSHINSKY LLP
STREET: 2101 L Street N.W.
                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:

NAME: Brady, Jr., James W.

REGISTRATION NUMBER: 32,115

REFERENCE/DOCKET NUMBER: 28280.016/P016

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-887-0689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy (
COMPUTER: IBM PC com)
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                                                    MOLECULE TYPE:
                                                                      TOPOLOGY: lir
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ZIP: 20037
                  NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Washington
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elen M.
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Best Local Similarity
Matches 440; Conserv
                     631 TATCTCCAAACGATAAACGGAGTTTTAC 658
                                                                361
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TATCTCCAAACGATAAACGGANTTNTAC 448
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Pred. No. 9.8e-89;
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US-08-560-007B-4 Sequence 4, Application US/08560007B
Patent No. 5914248
GENERAL INFORMATION:
APPLICANT: KUIPERS, OSCAR PAUL
APPLICANT: DE VOS, WILLEM MEINDERT
TITLE OF INVENTION: METHOD FOR CONTROLLING THE GENE
TITLE OF INVENTION: EXPRESSION IN LACTIC ACID BACTERIA CLASSIFICATION: 435
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS: SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/560,007B
FILING DATE: 17 NOV 1995 COMPUTER READABLE FORM: MEDIUM TYPE: FLOPPY DISK CORRESPONDENCE ADDRESS:
ADDRESSEE: THE WEBB LAW FIRM
STREET: 700 KOPPERS BUILDING, NUMBER OF SEQUENCES: COMPUTER: NEC 286 OPERATING SYSTEM: CITY: PITTSBURGH STATE: PENNSYLVANIA STRANDEDNESS: TOPOLOGY: LENGTH: COUNTRY: 15219-1818 NUCLEIC ACID UNITED STATES OF UNKNOWN NEC 286 SOG 4: AMERICA 436 SEVENTH AVENUE

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US-08-129-151A-1
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Vere
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/129,151A
FILING DATE: 07-OCT-1993
CLASSIFICATION DATA:
APPLICATION NUMBER: NL 9100634
FILING DATE: 11-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: NL 9100634
FILING DATE: 11-APR-1991
PRIOR APPLICATION NUMBER: PCT/NL92/00068
FILING DATE: 09-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: PATCH, ANDRER: 32,925
REFERENCE/DOCKET NUMBER: BO 37078
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: DE VOS, Willem M.
APPLICANT: SIEZEN, Roelant J.
APPLICANT: KUIPERS, OSCAT P.
TITLE OF INVENTION: LANTIBIOTICS SIMILAR TO NISIN A, LACTIC
TITLE OF INVENTION: ACID BACTERIA WHICH PRODUCE SUCH LANTIBIOTICS, METHOD FOR
TITLE OF INVENTION: CONSTRUCTING SUCH LACTIC ACID BACTERIA AND METHOD FOR
TITLE OF INVENTION: PRESERVING FOODSTUFFS WITH ETC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: U
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                                                                                                                                                                                                                                                                                                                                                                                                                                           745 South
                                                                                                                                                                                                                                                                                                                                                                                       USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                        THOMPSON
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0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Second
                                                                                                                                                                                                                                                                           Version
                                                                                                                                                                                                                                                                                                                                                                                                                                           Floor
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Best Local Simi
Matches 359;
                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Appli
Patent No. 592894
GENERAL INFORMAT
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/715,579
FILING DATE: 19-SEP-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 703/685-0573
TELEX: 248425 EMBON
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                               TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                        APPLICANT: 1
APPLICANT: 1
APPLICANT: 1
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                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY:
LOCATION:
                                                                                                                                                                      CITY: Arlington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
                                                                                                                                                               STATE:
                                                                                                                                                                                       STREET:
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                                                                                                                                              COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61
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                                                                                                                                              USA
                                                                                                                                                                                       745 South 23rd Street, S
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703/685-0573
                                                                                                                                                                                                                                                                                                                        SIEZEN,
                                                                                                                                                                                                                                                                                                         KUIPERS,
                                                                                                                                                                                                                                                                                                                                      DE VOS,
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3, Oscar P.
                                                                                                                                                                                                                                                                                                                                      Willem M.
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                                                                                                                                                                                                                                               LANTIBIOTICS SIMILAR TO NISIN A, LACTIC ACID BACTERIA WHICH PRODUCE SUCH LANTIBIOTICS, METHOD CONSTRUCTING SUCH LACTIC ACID BACTERIA AND METHOD FOR PRESERVING FOODSTUFFS WITH ETC.
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Pred. No. 9.5e-71;
0; Mismatches 1
                                                                                                                                                                                          Second Floor
                                                            Version
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                                                            #1.25
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FOR

PRIOR APPLICATION DATA:
APPLICATION NUMBER:

US 08/129,151

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RESULT 6
US-07-721-774A-1
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; LOCATION:
US-08-715-579-1
                                                                                                                                                       Sequence 1, Application US/07721774A Patent No. 5173297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 46.7%;
Best Local Similarity 99.7%;
Matches 359; Conservative
                         GENERAL INFORMATION:

APPLICANT: Vedamuthu, Ebenezer R; Henderson, James T;

APPLICANT: Maxugg, John D; van Wassenaar, Pieter D

TITLE OF INVENTION: No. 5173297el Bacteriocin From Lactococcus lactis

TITLE OF INVENTION: subspecies lactis

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:
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TELEX: 248425 EMBON
INFORMATION FOR SEQ ID NO: 1:
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: NL 9100634
FILING DATE: 11-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/NL92/000
FILING DATE: 09-APR-1992
ATTORNBY/AGENT INFORMATION:
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REGISTRATION NUMBER: 32,925
REFERENCE/DOCKET NUMBER: BO
TELECOMMUNICATION INFORMATION:
TELEPHONE: 701/521-2297
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            ADDRESSEE:
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2190
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121..294
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            Ian C. McLeod
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Pred. No. 9.5e-71;
0; Mismatches 1;
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US-07-882-715-1 | S-07-882-715-1 | Sequence 1, Application US/07882715 | Patent No. 5231165

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TELEX: NO. 51732976
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 321 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: Double
TOPOLOGY: Linear
MOLETIE TYPE: Other
                                                                                                                                                                                                                                                                                                                                                                                               Query Match 41.6%;
Best Local Similarity 99.7%;
                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:

NAME: Ian C. McLeod
REGISTRATION NUMBER: 20,931
REFERENCE/DOCKET NUMBER: MT 4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (517) 347-4100
TELEPAX: (517) 347-4103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HYPOTHETICAL: NO ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM AT
OPERATING SYSTEM: MS-DOS 5.0
SOPTWARE: ASCII text editor
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 48864
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Lactococcus
STRAIN: NRRL-B-18809
INDIVIDUAL ISOLATE: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CELL TYPE: unicellular organism
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                                                                   301
                               498
                                                           241
                                                                                            438
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                                                                                                                                                                                                                                                                                                                                                                                320; Conservative
                                                                                                                                                                                                                                                      61
GTTCAGACATGGATACTATCC
                GTTCAGACATGGATACTATCC 518
                                                              AACTTGTAATTGTAGTATTCACGTAAGCAAATAACCAAATCAAAGGATAGTATTTTGTTA
                                                                              AACTTGTCATTGTAGTATTCACGTAAGCAAATAACCAAATCAAAGGATAGTATTTTGTTA
                                                                                                                                             TTCGCTATGTACACCCCGGTTGTAAAACAGGAGCTCTGATGGGTTGTAACATGAAAAACAGC
                                                                                                                                                                                         CTTGGATTTGGTATCTGTTTCGAAGAAAGATTCAGGTGCATCACCACGCATTACAAGTAT
                                                                                                                                                                                                          CTTGGATTTGGTATCTGTTTCGAAGAAGATTCAGGTGCATCACCACGCATTACAAGTAT
                                                                                                                                                                                                                                                      TCGAAGGAACTACAAAATAAATTATAAGGAGGCACTCAAAATGAGTACAAAAGATTTTAA
                                                                                                                                                                                                                                                                          TCGAAGGAACTACAAAATAAATTATAAGGAGGCACTCAAAATGAGTACAAAAGATTTTAA 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              bacteriocin encoding DNA 101 to 271
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequencing
                                                                                                                                                                                                                                                                                                                                                                              Score 319.4; DB 1;
Pred. No. 3.8e-62;
0; Mismatches 1;
321
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Best Local Similarity 99.7%;
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 321 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Ian C. McLeod
REGISTRATION NUMBER: 20,931
REFERENCE/DOCKET NUMBER: MT 4.1-142
TELECOMMUNICATION INFORMATION:
TELEPHONE: (517) 347-4100
TELEFAX: (517) 347-4103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: 19920514
CLASSIFICATION: 435
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MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Ian C. McLead
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/721,774
FILING DATE: July 1, 1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OLECULE TYPE:
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OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: bacteriocin encoding DNA LOCATION: 101 to 271
                                                                                                                                                                                                                                                                                                                                                     IDENTIFICATION METHOD: sequencing
                                                                                                                                                                                                                                                                                                                                                                                                                    INDIVIDUAL ISOLATE: LLA-2.0 CELL TYPE: Unicellular organism
                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN: NRRL-B-18809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: NUCLEIC ACID
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                       378
                                                       121
                                                                                                                                                           258
                                                                                                                                                                                                                 198 CGCGAGCATAATAAACGGCTCTGATTAAATTCTGAAGTTTGTTAGATACAATGATTTCGT
                                                                                                                                                                                                                                                                320;
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TTCGCTATGTACACCCGGTTGTAAAACAGGAGCTCTGATGGGTTGTAACATGAAAACAGC
                                                                                 CTTGGATTTTGGTATCTGTTTCGAAGAAAGATTCAGGTGCATCACCACGCATTACAAGTAT 377
                                                                                                                                                         TCGAAGGAACTACAAAATAAATTATAAGGAGGCACTCAAAATGAGTACAAAAGATTTTAA 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Michigan
                                                                                                                         TCGAAGGAACTACAAAATAAATTATAAGGAGGCACTCAAAATGAGTACAAAAGATTTTAA
                                                                                                                                                                                             CGCGAGCATAATAAACGGCTCTGATTAAATTCTGAAGTTTGTTAGATACAATGATTTCGT
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                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lactococcus lactis subspecies lactis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ian C. McLeod
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Lactococcus lactis subspecies
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                                                                                                                                                                                                                                                                                Score 319.4; DB 1; Pred. No. 3.8e-62;
                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                Length 321;
                                                                                                                                                                                                                                                                Indels
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                                                                   US-07-882-079-1
Query Match
Best Local Similarity 99.
Matches 320; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                     TELEPAX: (517) 347-410
TELEX: No. 5232849e
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/721,
APPLICATION NUMBER: 07/721,
FILING DATE: July 1, 1991
ATTORNEY/AGENT INFORMATION:
NAME: IAN C. McLeod
REGISTRATION NUMBER: 20,931
REFERENCE/DOCKET NUMBER: MT
                                                                                                                                                                                                                                                                     TYPE: NUCLEIC ACID
STRANDEDNESS: Double
TOPOLOGY: 1.1-
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CITY: Okemos
TTATE: Michigan
TTSA
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                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: (517) 347-4100
TELEPAX: (517) 347-4103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOPTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/
FILING DATE: 19920514
CLASSIFICATION: 435
                                                                                                                  FEATURE:
NAME/KEY:
                                                                                                                                                                                                                    ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: Acer
OPERATING SYSTEM:
                                                                                                                                                     CELL TYPE:
                                                                                                                                                                                     STRAIN:
                                                                                                                                                                                                   ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE:
                                                                              NAME/KEY: bacteriocin encoding DNA LOCATION: 101 to 271
LOCATIFICATION METHOD: sequencing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
                                                                                                                                                                     INDIVIDUAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241 AACTTGTAATTGTAGTATTCACGTAAGCAAATAACCAAATCAAAGGATAGTATTTTGTTA 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 TTCGCTATGTACACCCGGTTGTAAAAACAGGAGCTCTGATGGGTTGTAACATGAAAAACAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               48864
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                                                                                                                                                                     NRRL-B-18809
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                                                                                                                                                                                                 Lactococcus lactis subspecies lactis
                                                                                                                                                    Unicellular organism
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                                                                                                                                                                                                                                                     No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Diskette, 5.25 inch, 360 Kb storage
             41.6%;
99.7%;
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Score 319.4; DB 1;
Pred. No. 3.8e-62;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          4.1 - 144
                                 Length 321;
   Indels
   0;
 Gaps
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Sequence 19. Application US/08836687B

PATENT NO. 6448034

GENERAL INFORMATION:
APPLICANT: Gasson, Michael John
APPLICANT: Dodd, Helen Mair
TITLE OF INVENTION: PRODUCTION OF VARIANT NISIN
FILE REFERENCE: 20747/70

CURRENT APPLICATION NUMBER: US/08/836,687B

CURRENT FILING DATE: 1995-11-20

NUMBER OF SEQ ID NOS: 51

SOFTWARE: PATENTIN Ver. 2.1

SEQ ID NO 19
LENGTH: 300

TYPE: DNA
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; Sequence 22, Application US/08836687B
               RESULT 10
US-08-836-687B-22
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 300;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Lactococcus sp
                                                                                                                                                                                                                     121
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                                                                                                                                                                                                                                                                                                     CTACAAAATAAATTATAAGGAGGCACTCAAAATGAGTACAAAAGGATTTTAACTTGGATTT
                                                                                                                                                                                                                                                                                                                                                                     TTGTAGTATTCACGTAAGCAAATAACCAAATCAAAGGATAGTATTTTGTTAGTTCAGACA
                                                                                                                                                                                                                   GGTATCTGTTTCGAAGAAAGATTCAGGTGCATCACCACGCATTACAAGTATTTCGCTATG
                                                                                                                                                                                                                                           GGTATCTGTTTCGAAGAAAGATTCAGGTGCATCACCACGCATTACAAGTATTTCGCTATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTTGGATTTGGTATCTGTTTCGAAGAAAGATTCAGGTGCATCACCACGCATTACAAGTAT 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCGAAGGAACTACAAAATAAATTATAAGGAGGCACTCAAAATGAGTACAAAAAGATTTTAA 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CGCGAGCATAATAAACGGCTCTGATTAAATTCTGAAGTTTGTTAGATACAATGATTTCGT
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                                                                                TTGTAGTATTCACGTAAGCAAATAACCAAATCAAAGGATAGTATTTTGTTAGTTCAGACA
                                                                                                                                                  TACACCCGGTTGTAAAACAGGAGCTCTGATGGGTTGTAACATGAAAACAGCAACTTGTCA
                                                                                                                                                                                TACACCCGGTTGTAAAACAGGAGCTCTGATGGGTTGTAACATGAAAACAGCAACTTGTCA
                                                                                                                                                                                                                                                                                    CTACAAAATAAATTATAAGGAGGCACTCAAAATGAGTACAAAAGATTTTAACTTGGATTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTTCAGACATGGATACTATCC 518
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                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                39.1%; Score 300; DB 4; 1
100.0%; Pred. No. 7.1e-58;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 300;
                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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                                                                                                                                                                                446
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                                                                                300
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APPLICANT: Gasson, Michael John
APPLICANT: Dodd, Helen Mair
TITLE OF INVENTION: PRODUCTION OF VARIANT NISIN
FILE REFERENCE: 20747/70
CURRENT APPLICATION NUMBER: US/08/836,687B
CURRENT FILING DATE: 1995-11-20
NUMBER OF SEQ ID NOS: 51
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 22
LENGTH: 300
TYPE: DNA
ORGANISM: Lactococcus sp.
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                                                                                                                                                                                                                                                          TITLE OF INVENTION: PRODUCTION OF VARIANT NISIN FILE REFERENCE: 20747/70 CURRENT APPLICATION NUMBER: US/08/836,687B CURRENT FILING DATE: 1995-11-20 NUMBER OF SEQ ID NOS: 51
SOFTWARE: Patentin Ver. 2.1
SEQ. ID NO 21
                                                                                                                                                                                                                                                                                                                                                                                           Sequence 21, Application US/08836687B Patent No. 6448034 GENERAL INFORMATION:
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Best Local Similarity
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GENERAL INFORMATION:
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TYPE: DNA
ORGANISM: Lactococcus
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Similarity 98.7%;
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Pred. No. 3.6e-57;
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RESULT 13

US-08-836-687B-25

Sequence 25, Application US/08836687B

Patent No. 6448034

GENERAL INFORMATION:
APPLICANT: Gasson, Michael John
APPLICANT: Dodd, Helen Mair
TITLE OF INVENTION: PRODUCTION OF VARIANT NISIN
FILE REFERENCE: 207477/70

CURRENT APPLICATION NUMBER: US/08/836,687B
CURRENT FILING DATE: 1995-11-20
NUMBER OF SEQ ID NOS: 51
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 25
LENGTH: 300
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US-08-836-687B-23

Sequence 23, Application US/08836687B

Patent No. 6448034

GENERAL INFORMATION:
APPLICANT: Gasson, Michael John
APPLICANT: Dodd, Helen Mair
ITILE OF INVENTION: PRODUCTION OF VARIANT NISIN
FILE REFERENCE: 20747/70

CURRENT APPLICATION NUMBER: US/08/836,687B

CURRENT FILING DATE: 1995-11-20

NUMBER OF SEQ ID NOS: 51

SOUTWARE: Patentin Ver. 2.1

SEQ ID NO 23

LENGTH: 300

TYPE: DNA
ORGANISM: Lactococcus sp.
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Best Local Similarity
Matches 296; Conserv
TYPE: DNA ORGANISM: Lactococcus sp.
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ilarity 98.7%;
Conservative
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Pred. No. 1.8e-56;
0; Mismatches 4
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TITLE OF INVENTION: PRODUCTION OF VARIANT NISIN
FILE REFERENCE: 20147/70
CURRENT APPLICATION NUMBER: US/08/836,687B
CURRENT FILING DATE: 1995-11-20
NUMBER OF SEQ ID NOS: 51
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 27
LENGTH: 300
TYPE: DNA
ORGANISM: Lactococcus sp.
US-08-836-687B-27
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                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
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Best Local Similarity
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Pred. No. 1.8e-56;
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RESULT 15 US-08-773-731A-3

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COUNTRY: USA
ZIP: 20037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/773,731A
FILING DATE: 24-DEC-1996
CLASSIFICATION ADATA:
APPLICATION NUMBER: US 08/313,123
FILING DATE: 18-NOV-1994
PRIOR APPLICATION NUMBER: US 08/313,123
FILING DATE: 18-NOV-1994
PRIOR APPLICATION NUMBER: US 08/313,123
FILING DATE: 01-APR-1993
PRIOR APPLICATION NUMBER: US 08/313,123
FILING DATE: 01-APR-1993
PRIOR APPLICATION NUMBER: 32,115
APPLICATION NUMBER: 32,115
APPLICATION NUMBER: 32,115
REGISTRATION NUMBER: 32,115
REGISTRATION NUMBER: 32,115
REFERENCE/DOCKET NUMBER: BE380.016/P016
FILEPHONE: 202-887-0689
INFORMATION: CHARACTERISTICS:
Search completed: January 12, 2004, 12:06:14 Job time: 69 secs
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                                                                                                                                                                                                                                                                                                                                                              ; TOPOLOGY: linear ; MOLECULE TYPE: DNA (genomic) US-08-773-731A-3
                                                                                                                                                                                                                                                                   Query Match 11.1%; Score 84.8; DB 3; Length 546; Best Local Similarity 97.7%; Pred. No. 2.4e-10; Matches 86; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3, Application US/08773731A Patent No. 6100056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Gasson, Michael J.
APPLICANT: Odd, Helen M.
TITLE OF INVENTION: NISINS
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE DICKSTEIN, SHAPIRO, MORIN & OSHINSKY LLP
STREET: 2101 L Street N.W.
                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 546 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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CITY: Washington
STATE: DC
                                                                                           519 AATAAATTATAAGGAGGCACTCAAAATG 546
                                                                                                                  273 AATAAATTATAAGGAGGCACTCAAAATG 300
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OM nucleic - nucleic search, using sw model
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48.4
48.2
48.2
47.2
      46.8
46.8
46.8
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seq length: 2000000000
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    7.0 11805
6.5 3673778
6.4 6361
6.3 13125
6.3 13125
6.3 4985
6.3 4985
6.3 17594
6.2 7351
6.1 5452
6.1 3673778
6.1 15303
6.1 17303
6.1 17403
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Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
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/cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
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/cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
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_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
  13 US-10-082-618-8

13 US-10-311-455-1721

18 13 US-10-312-841-1

13 US-10-311-455-1113

13 US-10-311-455-1200

13 US-10-240-485-110

13 US-10-056-405-10

13 US-10-094-240-10

15 US-10-094-240-10

15 US-10-094-240-12

10 US-10-311-455-129

11 US-10-311-455-122

12 US-10-311-455-122

13 US-10-311-455-122

14 US-10-311-455-959

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19 US-10-311-455-959
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Sequence 8, Appli
Sequence 1721, Ap
Sequence 113, Ap
Sequence 1100, Ap
Sequence 1100, Ap
Sequence 10, Appl
Sequence 10, Appl
Sequence 20, Appl
Sequence 2, Appli
Sequence 2, Appli
Sequence 2122, Ap
Sequence 2, Appli
Sequence 959, Ap
Sequence 2189, App
Sequence 959, App
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5.7	5.7	5.7	5.7	5.8	5.8	5.8	5.8	5.8	5.8	5.8	5.8	5.8	5.8	5.8	5.8	5.9	5.9	5.9	5.9	5.9	6.0	6.0	6.0	6.0	6.0	6.0	6.0	6.1	6.1
2000	12405	12405	8467	8801	8801	1088	6029	18624	13574	10006	7921	10716	755	755	17594	16287	5324	6904	6120	5511	13814	5987	5743	5689	5689	40862	16127	3673778	13123
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-09-938-842	-10-239-676	-10-240-453	-10-311-455	0-239-676	US-10-240-453-160	0-311-455	0-311-455-	0-311-455-	US-10-311-455-1290	-10-311-455-	0-311-455-	-10-311-455-139	0-027-632-	US-10-027-632-128109	-10-311-455	US-10-311-455-646	US-10-311-455-1763	-45	US-10-240-453-313	US-10-311-455-1843	US-10-311-455-1166	0-311-45	0-311-455-	0-23	US-10-240-453-100	0-31		US-10-312-841-2	.0-240-452-6
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## ALIGNMENTS

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APPLICANT: OLSTEIN, ALAN D.

APPLICANT: PERRTAG, JOSELEN

TITLE OF INVENTION: BACTERIOCIN-METAL COMPLEXES IN THE DETECTION OF

TITLE OF INVENTION: PATHOGENS AND OTHER BIOLOGICAL ANALYTES

FILE REFERENCE: 7005-0003

CURRENT APPLICATION NUMBER: US/10/082,618

CURRENT FILING DATE: 2002-02-22

NUMBER OF SEQ ID NOS: 8

SOFTWARE: PATENTIN Ver. 2.1

SEQ ID NO 8

LENGTH: 767

TYPE: DNA

ORGANISM: Streptococcus lactis

US-10-082-618-8
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US-10-082-618-8
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Publication No. US20030175207A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                Query Match 100.0%; Score 767; DB 13; Length 767; Best Local Similarity 100.0%; Pred. No. 3.6e-148; Matches 767; Conservative 0; Mismatches 0; Indels 0
                            181
                                                                              121
                                                                                                                           121 AATAGAAACATTAACAAATCTAAAACAGTCTTAATTCTATCTTGAGAAAGTATTGGTAAT 180
                                                                                                                                                                                  61
                                                                                                                                                                                                                               61 GAGATAGGTTTATTGAGTCTTAGACATACTTGAATGACCTAGTCTTATAACTATACTGAC 120
                                                                                                                                                                                                                                                                                                           1 AGTTGACGAATATTTAATAATTTTAATAATATCTTGATTTTCTAGTTCCTGAATAATATA 60
AATATTATTGTCGATAACGCGAGCATAATAAACGGCTCTGATTAAATTCTGAAGTTTGTT 240
                                                                                                                                                                                GAGATAGGTTTATTGAGTCTTAGACATACTTGAATGACCTAGTCTTATAACTATACTGAC
                                                                              AATAGAAACATTAACAAATCTAAAACAGTCTTAATTCTATCTTGAGAAAGTATTGGTAAT 180
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US-10-311-455-1721
; Sequence 1721, Application US/10311455
; Publication No. US20030143606A1
; GENERAL INFORMATION:
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                                                                                                               US-10-311-455-1721
                                                                                                                                                           NUMBER OF SEQ ID NOS: 2424
SEQ ID NO 1721
LENGTH: 11805
TYPE: DNA
ORGANISM: Artificial Sequence
                                                Matches 162;
                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: PCT/EP01/07537
PRIOR FILING DATE: 2001-07-02
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-09-01
                                                                                                                                                                                                                                                                                                                                       APPLICANT: OLEK, Alexander
APPLICANT: PIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determ
TITLE OF INVENTION: Cyrosine methylation
FILE REFERENCE: 5013.1014
CURRENT APPLICATION NUMBER: US/10/311,455
CURRENT FILING DATE: 2002-12-16
                                                                                                                           FEATURE: OTHER INFORMATION: chemically treated genomic DNA
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                  12
ATTTAATAATTTTAATAATATCTTGATTTTCTAGTTCCTGAATAATATAGAGATAGGTTT 71
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AATATTATTGTCGATAACGCGAGCATAATAAACGGCTCTGATTAAATTCTGAAGTTTGTT
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                                              Score 53.4; DB 13;
Pred. No. 0.61;
0; Mismatches 181;
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                                                                              Length 11805;
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; NAME/KEY: unsure
; LOCATION: (3294164)
US-10-312-841-1
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US-10-312-841-1
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Best Local Similarity
Matches 134; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Epigenomics AG
TITLE OF INVENTION: Diagnose von bedeutenden
FILE REFERENCE: BO1/1208/WO
CURRENT APPLICATION NUMBER: US/10/312,841
CURRENT FILING DATE: 2002-12-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE: OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 3673778
TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                 2686816 AATGTGTTATATATATATTATGGAATATTATGTAGTTATGAAAAAGAATGAGTTTATGTT
                                                                                                                                                                  2686756 TTTGTAGAATTTATAAAGAAATGATGGGGAAAATATATTAAAGATAGAGTGGATAAAGTA
                                                                                                                                                                                                                                  2686696 GTTAAGAGGTTATTAATATAGATATTTATTTATGGATATGCGAGATTGTTGTTTATTTTT
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                                                                                                                                                                                           GCTAAATAGCTTATAAAAATAAAGAGAGGAGAAAAAACATGATAAAAAGTTCATTTAAAGCT
                                                                                                                                                                                                                                                          GATAGTATTTTGTTAGTTCAGACATGGATACTATCCTATTTTTATAAGTTATTTAGGGTT
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                                  TATACTCAAGTCATTGAGACTGTAAGTAAAAATAAAGTTTTTTTGGAACAGTTACTACTA
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; Pred. No. 29;
0; Mismatches
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RESULT 4 US-10-311-455-1113 ; Sequence 1113, A

Application US/10311455

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FILE REFERENCE: 5013.1014

CURRENT APPLICATION NUMBER: US/10/311,455

CURRENT FILING DATE: 2002-12-16

PRIOR APPLICATION NUMBER: PCT/EP01/07537

PRIOR FILING DATE: 2001-07-02

PRIOR APPLICATION NUMBER: DE 10032529.7

PRIOR FILING DATE: 2000-06-30

PRIOR PILING DATE: 2000-06-30

PRIOR APPLICATION NUMBER: DE 10043826.1

PRIOR APPLICATION NUMBER: DE 10043826.1

PRIOR FILING DATE: 2000-09-01

NUMBER OF SEQ ID NOS: 2424

SEQ ID NO 1113

SEQ ID NO 1113
APPLICANT: BERLIN, KUIT
TITLE OF INVENTION: Diagnosis of Diseases As:
TITLE OF INVENTION: Cytosine methylation
FILE REFERENCE: 5013.1014
CURRENT APPLICATION NUMBER: US/10/311,455
CURRENT FILING DATE: 2002-12-16
PRIOR APPLICATION NUMBER: PCT/EP01/07537
PRIOR FILING DATE: 2001-07-02
PRIOR FILING DATE: 2001-07-02
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: DE 1003529.7
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR APPLICATION NUMBER: DE 10043826.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: OLEK, Alexander
APPLICANT: PIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determ
TITLE OF INVENTION: Cytosine methylation
                                                                                                                                                                                                                                                          APPLICANT: OLEK, Alexander APPLICANT: PIEPENBROCK, Christian APPLICANT: BERLIN, Kurt
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                                                                                                                                                                                                                                     Associated with the
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OTHER INFORMATION: chemically treated genomic FEATURE:
NAME/KEY: unsure
LCCATION: 11070, 11234
OTHER INFORMATION: n is a or g or c or t US-10-311-455-1200
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SEQ ID NO 1200
LENGTH: 13125
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Best Local Similarity 46.9%;
Matches 151; Conservative
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TYPE: DNA
ORGANISM: Artificial Sequence
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                             TAGCTAATCCTAAACTCTATGA 742
                                                                                                                                        CTCAACCGTTTTTAGTAAGAAATACAATTTTATCTCCAAACGATAAACGGAGTTTTACTG 660
                                                                                                                                                                                                            TTGCTAAATAGCTTATAAAAATAAAGAGAGAAAAAACATGATAAAAAGTTCATTTAAAG 600
                                                                                                                                                                                                                                          ACATTACTTAAAACAAAAACAAAAAATTATATATAAATTTAAATTTAAATACATATATCTCA 2020
                                                           TTATTAACTTATTAACCCAACTTAACAAAATAAAAAACCAAAATAAAACTCAAACCTAAAA 1960
CAACCTATCAAACTCTCTATAA 1818
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Pred. No. 6.8;
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US-10-240-485-110/c

Sequence 110, Application US/10240485

Publication No. US20030148327A1

GENERAL INFORMATION:
APPLICANT: OLEK, Alexander
APPLICANT: DIEDENBROCK, Christian
APPLICANT: BERLIN, Kurt

TITLE OF INVENTION: Diagnosis of Diseases Associated with
TITLE OF INVENTION: Metastasis
FILE REFERENCE: 5013.1007

CURRENT APPLICATION NUMBER: US/10/240,485

CURRENT FILING DATE: 2002-10-02

PRIOR APPLICATION NUMBER: DE 10019058.8

PRIOR APPLICATION NUMBER: DE 10019058.8

PRIOR FILING DATE: 2000-04-06

PRIOR PRICH DATE: 2000-04-06

PRIOR FILING DATE: 2000-04-07

PRIOR FILING DATE: 2000-04-07

PRIOR FILING DATE: 2000-06-30

PRIOR APPLICATION NUMBER: DE 10032529.7

PRIOR APPLICATION NUMBER: DE 10032529.7

PRIOR APPLICATION NUMBER: DE 10043826.1

PRIOR APPLICATION NUMBER: DE 10043826.1

PRIOR APPLICATION DATE: 2000-09-01

NUMBER OF SEQ ID NOS: 202

SEO ID NO 110

LENGTH: 13125

TYPE: DNA

ORGANISM: Artificial Sequence
FEATURE:

OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
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APPLICANT: ZWIEBEL, LAURENCE J.
TITLE OF INVENTION: MOSQUITO OLFACTORY GENES, PO
TITLE OF INVENTION: USE THEREOF
FILE REFERENCE: N7841
CURRENT FILING DATE: 2002-01-24
PRIOR APPLICATION NUMBER: 60/264,649
PRIOR APPLICATION NUMBER: 60/264,649
PRIOR FILING DATE: 2001-01-26
NUMBER OF SEQ ID NOS: 23
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 10
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Sequence 10, Application US/10056405
Publication No. US20030166013A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                              ; LENGTH: 4985
; TYPE: DNA
; ORGANISM: Anopheles gambiae
US-10-056-405-10
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                                                                                                                                                                                                                                                                                      Query Match 6.3%;
Best Local Similarity 47.0%;
Matches 149; Conservative
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Best Local Similarity 46.9%;
Matches 151; Conservative
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                                                                                                                                                                             61 GAGATAGGTTTATTGAGTCTTAGACATACTTGAATGACCTAGTCTTATAACTATACTGAC 120
                                                                     AATAGAAACATTAACAAATCTAAAACAGTCTTAATTCTATCTTGAGAAAGTATTGGTAAT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TAGCTAATCCTAAACTCTATGA 742
                                AATATTATTGTCGATAACGCGAGCATAATAAACGGCTCTGATTAAATTCTGAAGTTTGTT 240
                                                                                                                                                                                                                                                    AGTTGACGAATATTTAATAATTTAATATATCTTGATTTTCTAGTTCCTGAATAATATA 60
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                                                                                                                                                                                                                                                                                      Score 48.2; DB 13;
Pred. No. 5.1;
0; Mismatches 168;
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US-10-311-455-1999

Sequence 1999, Application US/10311455

Sequence 1999, Application US/10311455

Publication No. US20030143606A1

GENERAL INFORMATION:
APPLICANT: PIEDENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with
TITLE OF INVENTION: Cytosine methylation
FILE REFERENCE: 5013.1014

CURRENT APPLICATION NUMBER: US/10/311,455

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Immune

System

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Determi

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FILE REFERENCE: N8289

CURRENT APPLICATION NUMBER: US/10/094,240

CURRENT FILING DATE: 2001-03-08

PRIOR APPLICATION NUMBER: 10/056,405

PRIOR FILING DATE: 2002-01-24

PRIOR APPLICATION NUMBER: 60/264,649

PRIOR FILING DATE: 2001-01-26

NUMBER OF SEQ ID NOS: 27

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 10
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US-10-094-240-10/c
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                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 6.3%;
Best Local Similarity 47.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: ZWIEBEL, LAURENCE J.
TITLE OF INVENTION: ARRESTIN GENE, POLYPEPTIDE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Anopheles gambiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 4985
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                                             AATATTATTGTCGATAACGCGAGCATAATAAACGGCTCTGATTAAATTCTGAAGTTTGTT 240
          AGTACAAAAGATTTTAA 317
                                                                             AGATACAATGATTTCGTTCGAAGGAACTACAAAATTAAATTATAAGGAGGCACTCAAAATG 300
                                                                                                                  AATAATAATAATAA 2364
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                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches 168;
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Burnathen Charles

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CURRENT FILING DATE: 2002-12-16
PRIOR APPLICATION NUMBER: PCT/EP01/07537
PRIOR FILING DATE: 2001-07-02
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 2424
SEQ ID NO 1999
LENGTH: 17594
TYPE: DNA
ORGANISM: Artificial Sequence
PERITIE:
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; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-311-455-1999
                                                                                                                                                APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determ
TITLE OF INVENTION: Cytosine methylation
FILE REFERENCE: 5013.1014
CURRENT FILING DATE: 2002-12-16
PRIOR PELICATION NUMBER: US/10/311,455
CURRENT FILING DATE: 2002-12-16
PRIOR APPLICATION NUMBER: PCT/EP01/07537
PRIOR FILING DATE: 2001-07-02
PRIOR FILING DATE: 2001-07-02
PRIOR FILING DATE: 2001-07-07
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 2424
SEQ ID NO 2
LENGTH: 7351
 Query Match 6.2%;
Best Local Similarity 48.8%;
Matches 160; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/10311455
Publication No. US20030143606A1
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                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: OLEK, Alexande APPLICANT: PIEPENBROCK, APPLICANT: BERLIN, Kurt
                                                                                                    TYPE: DNA ORGANISM: Artificial Sequence FEATURE:
                                                                                    OTHER INFORMATION: chemically treated genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity hes 138; Conser
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Score 47.2; DB 13;
Pred. No. 9.5;
0; Mismatches 163;
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Pred. No. 9.2;
0; Mismatches 150;
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                              Length 7351;
                                                                                    (Homo sapiens)
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; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens) US-10-311-455-1122
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GENERAL INFORMATION
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Publication No. US20030143606A1
                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 1122
                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determi TITLE OF INVENTION: Cytosine methylation FILE REFERENCE: 5013.1014

CURRENT APPLICATION NUMBER: US/10/311,455

CURRENT FILING DATE: 2002-12-16

PRIOR APPLICATION NUMBER: PCT/EP01/07537

PRIOR PILING DATE: 2001-07-02

PRIOR APPLICATION NUMBER: DE 10032529.7

PRIOR APPLICATION NUMBER: DE 10043826.1

PRIOR PILING DATE: 2000-06-30

PRIOR PILING DATE: 2000-09-01

PRIOR FILING DATE: 2000-09-01

PRIOR FILING DATE: 2000-09-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: PIEPENBROCK, Christian APPLICANT: BERLIN, Kurt
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 5452
TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
                                                                                                     124 АGAAACATTAACAAATCTAAAACAGTCTTAATTCTATCTTGAGAAAGTATTGGTAATAAT 183
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ATTATTGTCGATAACGCGAGCATAATAAACGGCTCTGATTAAATTCTGAAGTTTGTTAGA 243
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Pred. No. 9.3;
0; Mismatches 350
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; NAME/KEY: unsure
; LOCATION: (379615)
US-10-312-841-2
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US-10-312-841-2/c
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Publication No. US20030186277A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                 Query Match
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TITLE OF INVENTION: Diagnose von bedeutenden genetischen Parametern innerhalb des MHC
FILE REFERENCE: BO1/1208/WO
CÜRRENT APPLICATION NUMBER: US/10/312,841
CURRENT FILING DATE: 2002-12-30
NUMBER OF SEQ ID NOS: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 3673778
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
                                             1227150
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les 134; Conser
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TTTTTTGGAACAGTTACTAGCTAATCCTAAACTCTA 739
                                             АСТССАЛАСТАРАССАРАРАСВАТАСССТАТТТСРАРАВЛАРАРАРАВЛЕЙАЙАТАРАВ 1227091
                                                                                                      AATAAAAAATTACTTAAACCCAAAAAATTATAACTACAATAAACCATTTATACCACTAC
                                                                                                                                 GATAAAAAGTTCATTTAAAGCTCAACCGTTTTTAGTAAGAAATACAATTTTATCTCCAAA
                                                                                                                                                                                                                          TATACCAAATAAAATACGAAAAAATTCATTTTAAAAAACTTACAATTTAATACAAACAAA
                                                                                                                                                                                                                                                         TAAGCAAATAACCAAATCAAAGGATAGTATTTTGTTAGTTCAGACATGGATACTATCCTA
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                                                                         TTTTTATAAGTTATTTAGGGTTGCTAAATAGCTTATAAAAATAAAGAGAGGAAAAAACAT
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                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                        chemically treated genomic DNA
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                                                                                                                                                                                                                                                                                                   Score 47;
Pred. No.
                                                                                                                                                                                                                                                                                     ed. No. 1.1e+02;
Mismatches 145
                                                                                                                                                                                                                                                                                                                 DB 13; Length 3673778;
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Best Local Similarity 49.6
'.~ 120; Conservative
                                                                                                                                                                            Sequence 959, Application US/10311455
Publication No. US20030143606A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Publication No. US20030143606A1 GENERAL INFORMATION:
                                                                                                                                    APPLICANT:
                                                                                                                                               APPLICANT: OLEK, Alexander APPLICANT: PIEPENBROCK, Cl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 2424
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APPLICANT: PIEPENBROCK, Christian
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OTHER INFORMATION:
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 FILING DATE: 2000-06-30
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APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases As;
TITLE OF INVENTION: Cytosine methylation
FILE REFERENCE: 5013.1014
CURRENT APPLICATION NUMBER: US/10/311,455
CURRENT FILING DATE: 2002-12-16
PRIOR APPLICATION NUMBER: PCT/EP01/07537
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR APPLICATION NUMBER: DE 10032529.7
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PRIOR FILING DATE: 2001-07-02
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-09-01
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TITLE OF INVENTION: Diagnosis of Diseases
TITLE OF INVENTION: cytosine methylation
FILE REFERENCE: 5013.1014
CURRENT APPLICATION NUMBER: US/10/311,455
CURRENT FILING DATE: 2002-12-16
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Pred. No. 10;
                                                                                                                                                                                              Associated with the
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PRIOR APPLICATION NUMBER: PCT/EP01/07537
PRIOR FILING DATE: 2001-07-02
PRIOR PPLICATION NUMBER: DE 10032529.7
PRIOR PILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 2424
SEQ ID NO 2189
LENGTH: 7403
TYPE: DNA
ORGANISM: Artificial Sequence
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PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 2424
SEQ ID NO 959
LENGTH: 17294
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
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                                                                                                                           Query Match
6.1%; Score 46.6;
Best Local Similarity 48.9%; Pred. No. 13;
Matches 158; Conservative 0; Mismatches
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Best Local Similarity 47.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Detern TITLE OF INVENTION: Cytosine methylation FILE REFERENCE: 5013.1014
CURRENT APPLICATION NUMBER: US/10/311,455
CURRENT FILING DATE: 2002-12-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: OLEK,
APPLICANT: PIEPE
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64 ATAGGTTTATTGAGTCTTAGACATACTTGAATGACCTAGTCTTATAACTATACTGACAAT 123
                                                                TGACGAATATTTAATAATTATTAATATCTTGATTTTCTAGTTCCTGAATAATATATAGAG
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                                      TCATTAAATTTCCTTCATTTTATTACTTTTTACATTTTATTTTATCTTTTTAAAATACAC 4391
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Search completed: January 12, 2004, 14:02:55 Job time : 928 secs THIS PAGE BLANK (USPTG)

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Result
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## ALIGNMENTS

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Collaboration with the Berkeley Drosophila (Enome Project (BDGP) and the BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Oscegawa and Mammoser in Pieter de Jong's laboratory in the Department of	BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr - Web : www.genoscope.cns.fr) Determination of this BAC-end sequence was carried out as part of a	Direct Submission Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :	1 (bases 1 to 1101) Genoscope.	Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.	Drosophila melanogaster (fruit fly) Drosophila melanogaster	AL069706.1 GI:4949849 GSS.	fly), genomic survey sequence. AL069706	la melanogaster genome survey sequence T7 en 3 of RPCI-98 library from Drosophila melanoo	CNSOOEVL 1101 bp DNA linear GSS 04-JUN-1999

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Drosophila melanogaster genome survey sequence TET3 end of BACRO8K10 of RPCI-98 library from Drosophila melanogaster
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|mol_type="genomic_DNA"
|/db_xref="taxon:7227"
|/clone="BACR29B23"
|/clone_lib="RPCI-98"
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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Direct Submission
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/mol_type="genomic DNA"
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/db_xref="taxon: 7227"
/clone="BACRO8K10"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Unpublished
This sequence was generated from the SP6 end of BAC 108G13. 108G13 is part of the Daniokey BAC Library created by R. Plasterk and N.V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (27-JAN-2003) The Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Actinopterygii; Neopterygii; Teleostei; Cypriniformes; Cyprinidae; Danio.
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Danio rerio
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BX145762
BX145762.1 GI:27977115
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                                                                                         CATTAACAAATCTAAAACAGTCTTAATTCTATCTTGAGAAAGTATTGGTAATAATAATATTAT 188
                                                                                                                                       TTTATTGAGTCTTAGACATACTTGAATGACCTAGTCTTATAACTATACTGACAATAGAAA 128
TATTAATAATAATAATAACGTTAACAGTAGTTATAAAATTAATAATAATAATAAAAT
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Inbrary was constructed by Life Technologies, a division of
Invitrogen. Contact: Feng Liang Email: fliang@lifetech.com |
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSOCAPOOBCA01QP1.
Location/Qualifiers
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Genoscope - Centre National de Sequencage
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                   TATTGAGTCTTAGACATACTTGAATGACCTAGTCTTATAACTATACTGACAATAGAAACA 130
                                                                                                                                                                       TATTTAATAATTTTATTAATATCTTGATTTTCTAGTTCCTGAATAATATAGAGATAGGTT 70
                                                                                                                                       TATWWWWDDDDAKAWADAGAATWTTTTTTWWRAGRGARKRDGTTDTRAADWWWWTWAAW 431
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/clone lib="Homo sapiens THYMUS"
/clone lib="Homo sapiens THYMUS"
/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned i the Not I and ECORV sites of the pCMVSPORT 6 vector. Library was not normalized."

1 30 c 71 g 310 t 274 others
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/mol_type="mRNA"
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/clone="CS0CAP008YB01"
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Homo sapiens cDNA clone
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                                                                                         Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
BR 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. Contact : Feng Liang Email : fliang@lifetech.com |
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSOCAP008BE02QP1.
                                                                                                                                                                                                Bukaryota; Metazoa; Chordata; Craniata; Vert-
Mammalia; Eutheria; Primates; Catarrhini; Ho
1 (bases 1 to 1200)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-ength CDNA libraries and normalization
Unpublished
                                                                                                                                                                                                                                                                                                                                              BX415878 Homo sapiens THYMUS 5-PRIME, mRNA sequence.
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSOCAP008YI04"
/tissue_type="THYMUS"
                                                       organism="Homo sapiens"
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AL536104 Homo sapiens FETAL BRAIN Homo sapiens
CSODF022YC18 5-PRIME, mRNA sequence.
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AL536104.2 GI:31260974
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/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-cligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned ithe Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized."

70 c 85 g 447 t 170 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: segref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. Contact: Feng Liang Email: fllang@ilfetech.com
http://fulllength.invitrogen.com/ Invitrogen
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization
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Location/Qualifiers
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                                                                                                                                                                               TATATAWTAWGWRTAAATAWWWWTAWAAWATWTATWTAAAAAWAWAATWWAAATATWWTT
                                                                                                                                                                                                             GTTGTAACATGAAAAACAGCAACTTGTCATTGTAGTATTCACGTAAGCAAATAACCAAAATC 478
                                                                                                                                                                                                                                                                           CACCACGCATTACAAGTATTTCGCTATGTACACCCGGTTGTAAAACAGGAGCTCTGATGG 418
                                                                                                                                                                                                                                                                                                                                                                           ATAWTTTATRWWATWATWTTWWTWTTWTTWKATTAATWATAATWWTAAWWTTTTWTATT 830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AMTATATTOWWTTATATAADTDTATATAAATTTWTTATWTWTTTTATTTTTWTWTATTTT 710
AGCTCAACCGTTTTTAGTAAGAAATACAATTTTATCTCCAAACGATAAACGGAGTTTTAC 658
                                                  ATAATATTATTGTCGATAACGCGAGCATAATAAACGGCTCTGATTAAATTCTGAAGTTTG
                                                                                                                ATWATTWTTTTTWTWTTTWWATWSTATWATAAAAWTAWTWTTTTTTAATWTAWATAWTWT
                                                                                                                                               AAAGGATAGTATTTTGTTAGTTCAGACATGGATACTATCCTATTTTTATAAGTTATTTAG
                                                                                                                                                                                                                                             TTTATWTTTTTATTATAAWTTTWTAWAWWATTWTWWWWAATWATTAGWTAWWAWWAWAA
                                                                                                                                                                                                                                                                                                             WTAWTAWAAAWWTTTWATATTWWTATTTTTWATAAATTTATT---WTTTTAATTTTTAAW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACAATAGAAACATTAACAAATCTAAAACAGTCTTAATTCTATCTTGAGAAAGTATTGGTA 178
                                                                             GGTTGCTAAATAGCTTATAAAAATAAAGAGAGGAAAAAACATGATAAAAAGTTCATTTAA 598
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone lib="Homo sapiens FETAL BRAIN"
/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDN/
was primed with a NotI-cligo(dT) primer. Five prime end
enriched, double-strand cDNA was digested with Not I and
cloned into the Not I and EcoRV sites of the pCMVSPORT 6
vector. Library was not normalized."
a 119 c 146 g 409 t 168 others
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODF022YC18"
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dev_stage="fetal"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 67.2; DE
Pred. No. 0.52;
94; Mismatches
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(bases 1 to 1056)
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АКАТАТААWAAAAAAAWAATATATAAAAAAAAAAWAAWTTTTGWAAWATGTTTTTTK 621
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/db xref="taxon:960;"
/clone="CSOCAPO04YG19"
/tissue type="THYMUS"
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                                                                                 al Similarity
163; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. Contact: Feng Liang Email: fliang@lifetech.com
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSODF022BB09QP1.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1201)

Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

Full length cDNA libraries and normalization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AL536104 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone CS0DF022YC18 5-PRIME, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                On Feb 13, 2001 this sequence version replaced Contact: Genoscope
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BP 191 91006 EVRY cedex - France
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ATWTATATATAAYMACTAWWWTAATATWAAAATHWTHTAWAAWATWTAATAATATCAAWW 1129
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                                    AAATCTAAAACAGTCTTAATTCTATCTTGAGAAAGTATTGGTAATAATATTATTGTCGAT 195
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                                                                                                                                                                                 359
                                                                               8.4%;
larity 32.8%;
Conservative
                                                                                                                                                                    /clone libe"Homo sapiens FETAL BRAIN"
/clone libe"Homo sapiens FETAL BRAIN"
/note="Organ: brain; Vector: pCMVSPORT_6; 1st strand cDNA
was primed with a NotI-oligo (dT) primer. Five prime end
enriched, double-strand cDNA was digested with Not I and
cloned into the Not I and EcoRV sites of the pCMVSPORT 6
vector. Library was not normalized."

119 c 146 g 409 t 168 others
                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODF022YC18"
                                                                                                                                                                                                                                                                                                                   tissue_type="FETAL BRAIN"
dev_stage="fetal"
                                                                             Score 64.6; DI
Pred. No. 1.3;
95; Mismatches
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Mammalia; Eutheria; P
1 (bases 1 to 1200)
Li,W.B., Gruber,C., J
                                                                                                                                                                                                                                                                                                                 Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. Contact: Feng Liang Email: fliang@lifetech.com URL
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BX415878 Homo sapiens THYMUS 5-PRIME, mRNA sequence.
                                                                                                                                                                                                                                                                          Faraday Avenue Genoscope sequence ID : CSOCAP008BE02QP1.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                              Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (human)
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                      428
              /tissue_type="THYMUS"
/clone_Tib="Nomo sabjens THYMUS"
/clone_Tib="Nomo sabjens THYMUS"
/note="Vector: pcMVSPORT 6; lst strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned i
the Not I and EcoRV sites of the pcMVSPORT 6 vector.
Library was not normalized."

170 c 85 g 447 t 170 others
                                                                                                                                                                            /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSOCAP008Y104"
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Hominidae;

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Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota, Metazoa; Arthropoda; Hexapoda; Inse
Neoptera; Endopterygota; Diptera; Brachycera;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1101)
                                                                                                                                                                                              CNS0039Q 1101 bp DNA linear GSS 03-JUN-1999 Drosophila melanogaster genome survey sequence TET3 end of BAC # BACR08M12 of RPCI-98 library from Drosophila melanogaster (fruit
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                                                                                                                                                                                                                                                                                                                               ATAAAATTAWATTTAWWWWATWTAAATWTAWTTTWTAW 1173
                                                                                                                                                                                                                                                                                                                                                                 GCTAATCCTAAACTCTATGATGTTATGCAGAAATATAAT 761
                                                                                                                                                                                                                                                                                                                                                                                                                                      TATACTCAAGTCATTGAGACTGTAAGTAAAAATAAAGTTTTTTTGGAACAGTTACTACTA 722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TWTATTTWWTWTAAAAAAATTATTTTTWTTAWAWTTTTWWTATATATTTAWTAAAATW
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ilarity 34.5%;
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Pred. No. 2.3;
5; Mismatches 390;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1098 WKDTGKRARRGARADAGAAAARAGRGDTTKTTTKWTWAAAAAAAAAAAAAKRAAAGRARAR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AL565455 Homo mapiens FETAL BRAIN Homo mapiens cDNA clone CSODF005YO18 3-PRIME, mRNA mequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
 AL565455
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                                                                                                                                                                                                                                                       AAAGTTCATTTAAAGCTCAACCGTTTTTAGTAAGAAATACAATTTTATCTCCAAACGATA
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                                                                                                                                                                                 WG----TTGRKTTTTTTWWAARTAAAAAAWAWTTWTKAAAAAAGKAAGTTAWTTWAAT 863
                                                                                                                                               <u>AAAWWAAWTGRWAAARTTTTTTTTTGGRRRRGRGRRRAAAAWTAKKGRGRRRDAAAAR</u>
                                                                                                                                                                                                                                                                                                                       ATAAGTTATTTAGGGTTGCTAAATAGCTTATAAAAATAAAGAGAGGAAAAAAACATGATAA 585
                                                                                                                                                                                                                                                                                                                                                                 WWTAWAWWAATKGDGGGRARGGGGGKTTTTTKWAAAAAAAAAAWTTTTTTTAAAATTTTT
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/note="end : TET3"
155 c 97 g
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/db_xref="taxon:7227"
/clone="BACR08M12"
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/mol_type="genomic DNA"
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34.9%; Pred. No. 2.7;
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Best Local Similarity
Matches 219; Conser
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Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 9232.f
more information about this cluster, see
http://www.genoscope.cns.fr/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1201)

Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

Full-length cDNA libraries and normalization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cgi-bin/cluster.cgi?seq=CSODF005BH09NF1&cluster=9232.f. Contact Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
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On Feb 16,
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EST.
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 AAAACAGCAACTTGTCATTGTAGTATTCACGTAAGCAAATAACCAAAATCAAAGGATAGTA 489
                                                            ACAAGTATTTCGCTATGTACACCCGGTTGTAAAACAGGAGCTCTGATGGGTTGTAACATG
                                                                                            GATTTCGTTCGAAGGAACTACAAATAAATTATAAGGAGGCACTCAAAATGAGTACAAAA 309
                                                                                                                                                                                                                   GTCGATAACGCGAGCATAATAAACGGCTCTGATTAAATTCTGAAGTTTGTTAGATACAAT
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                                                                                                                                                                                                                                                                                                                                                                                                     ATTAACAAATCTAAAACAGTCTTAATTCTATCTTGAGAAAGTATTGGTAATAATATTATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clome lib="Homo sapiens FETAL BRAIN"
/note="Organ: brain; Vector: pcWNSAPRT 6; 1st strand cDNA
was primed with a NotI-oligo(GT) primer. Five prime end
enriched, double-strand cDNA was digested with Not I and
cloned into the Not I and EcoRV stres of the pcWVSPORT 6
vector. Library was not normalized."
92 c 71 g 313 t 185 others
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/dev_stage="fetal"
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/mol_type="mRNA"
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/clone="CS0DF005YO18"
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Pred. No. 3.5;
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63 GATAGGTTTATTGAGTCTTAGACATACTTGAATGACCTAGTCTTATAACTATACTGACAA 122
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Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. Contact: Feng Liang Email: fliang@lifetech.com URL
http://fulllength.invitrogen.com/Invitro
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BX437758
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished
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                                                  TTATYTTAWTTTTTTTTYTTWTYTTYWCTTTTTTYTTTTATTTTTCTTWTTHIMTTCTTT 1138
                                                                                               TIGACGAATATITAATAATTTTATTAATATCITGATTTCTAGTTCCTGAATAATATAGA 62
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                                                                                                                                                                                                                                                                                  515
                                                                                                                                                    Conservative 127; Mismatches
                                                                                                                                                                                                                                                                       /mol_type="mRNA"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone="CSOCAP0089B01"
/tissue_type="THYMUS"
/clone Tib="Homo sapins THYMUS"
/clone Tib="Homo sapins THYMUS"
/note="Vector: pcMvSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pcMvSPORT 6 vector.
Library was not normalized."

30 c 71 g 310 t 274 others
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                     BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 9562.r
more information about this cluster, see
                                                                                                                   Unpublished
On Feb 15, 2001 this sequence version replaced
Contact: Genoscope
Contact: Genoscope
                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1201)

Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

Full-length cDNA libraries and normalization
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       http://www.genoscope.cns.fr/
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Web: www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part collaboration with the Berkeley Drosophila Genome Project (BDC The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila
                                                                                                                                                                                                         Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                  CNS00DKY 928 bp DNA linear GSS 04-JUN-1:
Drosophila melanogaster genome survey sequence T7 end of BAC #
BACR27A24 of RPCI-98 library from Drosophila melanogaster (fruit
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Feng Liang Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CS0DI001DC12QP1.
Location/Qualifiers
                                                                                                                   Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.f
                                                                                                                                                           Direct Submission
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/clone_Tib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="Ist strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
a 178 c 231 g 174 t 165 others
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/db_xref="taxon:9606"
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34.7%;
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Pred. No. 8;
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survey sequence T7 end of BAC #
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Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
BR 191 91006 EVRY cedex - France
Enail: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. Contact: Feng Liang Email: fliang@lifetech.com |
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 960)

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Pull-length cDNA libraries and normalization
Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the 1sogenic strain y2; cn bw sp, the same strain used for the BDGP's P1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                                       BX346155
BX346155.1
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                                                                                        Contact: Genoscope
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/note="end : T7"
70 c 84 g
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/mol_type="genomic DNA"
/db xrefe"taxon: 7227"
/clone="BACR27A24"
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Pred. No. 9
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CELLS (JURKAT CELL LINE) COT 10-NORM
CSODJ010YC14 5-PRIME, mRNA sequence.
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Similarity 35.1%;
ATCCTAAACTCTATGAT 743
                                            MMAMMATMAACCACCGTCTTCTTTAGAANACTGTTTTCTGGGATCTGATGTTAACCAGCC
                                                                                                                               GGTGAAATGTMAAMMMAGTAGTATCTGMMGTTTGAATTAGMTGMATAAMATATATTATA
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                                                                                                                                                                         CGTTTTTAGTAAGAAATACAATTTTATCTCCAAACGATAAACGGAGTTTTACTGAATATA 666
                                                                                                                                                                                                                 TAAMMMTTMAAATTAATAAWAMWAMAATMATATGTACMATGATTTGMMATGTCMAA
                                                                                                                                                                                                                                                              TAGCTTATAAAAATAAAGAGAGAAAAAAACATGATA--AAAAGTTCATTTAAAAGCTCAAC 606
                                                                                                                                                                                                                                                                                                      GAACTATTGCTGTGGGAARAAAGGMMTGATMATAAAAMTMATMTTCMTMATTAAGTAMMA
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100 c 80 g 366 t 130 others
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/cell_type="T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED"
/cell_line="JURKAT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'mol_type="mRNA"
'db_xref="taxon:9606"
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